

Query Match	100.0%;	Score 3237;	DB 2;	Length 604;
Best local Similarity	100.0%;	Pred. No. 1.6e-300;		
Matches 604;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```

QY 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGFQYKDCDCTRTGFGYGCSTPEFL 60
DB 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGFQYKDCDCTRTGFGYGCSTPEFL 60
QY 61 TRIKLFKPTPTVHYIILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
DB 61 TRIKLFKPTPTVHYIILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
QY 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDQGS 180
DB 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDQGS 180
QY 181 NMFAFAFHQFHTQFHTDHRKGPFTNGLGHVLDNHIYGETLARQRLRLFQDGMKY 240
DB 181 NMFAFAFHQFHTQFHTDHRKGPFTNGLGHVLDNHIYGETLARQRLRLFQDGMKY 240
QY 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGQEVFGIVPGIMMYATITLREHNRVCD 300
DB 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGQEVFGIVPGIMMYATITLREHNRVCD 300
QY 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFPDELLFNKQFOYQ 360
DB 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFPDELLFNKQFOYQ 360
QY 361 NR1AAEFNTLYHMHPLPPTFQIHDOKNYQOFIYNNLSILHEGITOQFVSEFTROLAGRV 420
DB 361 NR1AAEFNTLYHMHPLPPTFQIHDOKNYQOFIYNNLSILHEGITOQFVSEFTROLAGRV 420
QY 421 AGGRNVPAPVQKVSQASIDQSRQKYSFNEYRKRFLKYESFEELTGKEMSALEAL 480
DB 421 AGGRNVPAPVQKVSQASIDQSRQKYSFNEYRKRFLKYESFEELTGKEMSALEAL 480
QY 481 YGDIIDAVELYPALVVEKPRDAIFGETMVEVGAFFSLKGLMGVNICSPAYWKSTFGGEV 540
DB 481 YGDIIDAVELYPALVVEKPRDAIFGETMVEVGAFFSLKGLMGVNICSPAYWKSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 2
ID AAR72228 standard; protein: 604 AA.
XX
AC AAR72228;
XX
DT 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
DE Human cyclooxygenase-2.
XX
KW Cyclooxygenase-2; COX-2; COX-1; inhibitor; screening; osteosarcoma.
XX
OS Homo sapiens.
XX
PN W09509238-A1.
XX
PD 06-APR-1995.
XX
PE 13-SEP-1994; 94WO-CA000501.
XX
PR 27-SEP-1993; 93US-00084033.
XX
PA (MERI ) MERCK FROST CANADA INC.
XX
PI Oneil GP, Mancini JA;
XX
DR WPI; 1995-147436/19.

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DR N-PSDB; AA089376.
XX High level expression of human cyclooxygenase (COX)-2 - using new 3'
PT flanking region from COX-1, useful in assays for identifying potent,
PT selective or preferential inhibitors of COX-2.
XX Disclosure; Fig 1; 59pp; English.
XX Full-length cDNA derived from human osteosarcoma cells (given in
CC AA089376) encoded human COX-2 (AAR72228). High-level expression of COX-2
CC in COS7 cells was achieved using a vaccinia or baculovirus vector and a
CC construct in which COX-2 cDNA was attached at its 5' end to a 3' flanking
CC sequence of human COX-1 cDNA (AA089377). (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 604 AA;
Query Match 100.0%; Score 3237; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 1,66-300;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGFQYKDCDCTRTGFGYGCSTPEFL 60
DB 1 MLARALLICAVIALSHTANPCCSHPCCNRGYCMVGFQYKDCDCTRTGFGYGCSTPEFL 60
QY 61 TRIKLFKPTPTVHYIILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
DB 61 TRIKLFKPTPTVHYIILTHFKGFNNVNNIPFLNAINMSYVLTSSRLIDSPPTYNADY 120
QY 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDQGS 180
DB 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDQGS 180
QY 181 NMFAFAFHQFHTQFHTDHRKGPFTNGLGHVLDNHIYGETLARQRLRLFQDGMKY 240
DB 181 NMFAFAFHQFHTQFHTDHRKGPFTNGLGHVLDNHIYGETLARQRLRLFQDGMKY 240
QY 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGQEVFGIVPGIMMYATITLREHNRVCD 300
DB 241 QIIDGEMYPPTVKDQAEIYPPQVEHLRFVAGQEVFGIVPGIMMYATITLREHNRVCD 300
QY 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFPDELLFNKQFOYQ 360
DB 301 VLKQEHPEWGDQQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFPDELLFNKQFOYQ 360
QY 361 NR1AAEFNTLYHMHPLPPTFQIHDOKNYQOFIYNNLSILHEGITOQFVSEFTROLAGRV 420
DB 361 NR1AAEFNTLYHMHPLPPTFQIHDOKNYQOFIYNNLSILHEGITOQFVSEFTROLAGRV 420
QY 421 AGGRNVPAPVQKVSQASIDQSRQKYSFNEYRKRFLKYESFEELTGKEMSALEAL 480
DB 421 AGGRNVPAPVQKVSQASIDQSRQKYSFNEYRKRFLKYESFEELTGKEMSALEAL 480
QY 481 YGDIIDAVELYPALVVEKPRDAIFGETMVEVGAFFSLKGLMGVNICSPAYWKSTFGGEV 540
DB 481 YGDIIDAVELYPALVVEKPRDAIFGETMVEVGAFFSLKGLMGVNICSPAYWKSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPPELIKTVTINASSRSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 3
ID AAB72199 standard; protein: 604 AA.
XX
AC AAB72199;
XX
DT 02-MAY-2001 (first entry)

```

XX DE Human prostaglandin-endoperoxide synthase 2 (PTGS2) protein.  
 XX KW Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;  
 KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;  
 XX inflammation.  
 XX OS Homo sapiens.  
 XX FT Key location/Qualifiers  
 FT Misc-difference 587 /note="Optionally Arg when variation occurs in DNA  
 FT sequence due to single nucleotide polymorphism"  
 XX MO200107662-A1.  
 XX PD 01-FEB-2001.  
 XX PF 24-JUL-2000; 2000WO-US020114.  
 XX PR 22-JUL-1999; 99US-0145170P.  
 XX PA (GENA-) GENAISSANCE PHARM INC.  
 XX PT Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;  
 DR WPI; 2001-182805/18.  
 XX N-RSDB; AAF80896, AAF80897.  
 PT New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,  
 PT for gene therapy of inflammation and for establishing a genotype or  
 PT haplotype.  
 PS Claim 10; Fig 3; 118bp; English.  
 XX This invention relates to a polynucleotide sequence that is a polymorphic  
 CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene  
 CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence  
 CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and  
 CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2  
 CC protein is represented by AAF872199. The invention includes PCR and  
 CC sequencing primers, and probes represented in AAF80898 - AAF81151 which  
 CC are used to isolate and characterize the PTGS2 gene sequence, and to  
 CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide  
 CC sequences are used to express variant PTGS2 proteins, for structural  
 CC analysis or drug-binding studies and also in gene therapy (either  
 CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are  
 CC useful for diagnosis, prognosis and therapy and analysis of the new, and  
 CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,  
 CC especially for determining association between a particular trait, e.g. a  
 CC clinical response to drugs that target PTGS2 but also disease  
 CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly  
 CC used for developing diagnostic tests and treatments for immune-related  
 CC disorders such as arthritis and inflammation. The polymorphisms may also  
 CC be used to study expression and biological function of PTGS2. Transgenic  
 CC animals that express PTGS2 are used to study expression of PTGS2  
 CC isoforms, for in vivo drug screening and testing, and for assessing  
 CC effects of therapeutic agents  
 XX SQ Sequence 604 AA;  
 Query Match 100.0%; Score 3237; DB 4; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-300;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLARALLICAVLAISHTANPCSCSHPCQNRGVCMGVGFQYKDCDRTGFGYGENCSTPEFL 60  
 DB 1 MLARALLICAVLAISHTANPCSCSHPCQNRGVCMGVGFQYKDCDRTGFGYGENCSTPEFL 60  
 QY 61 TRIKLFLKPTNTVHYIILTHKGFNNVNNIPLRLNALMSYVLTSSHLIDSPPTYNDY 120  
 DB 61 TRIKLFLKPTNTVHYIILTHKGFNNVNNIPLRLNALMSYVLTSSHLIDSPPTYNDY 120

QY 121 GYKSWFAFNSLSTYTRALPVVDDCPPTLGVKQKQPLDSNEIYKLLRRKFFIPDPGS 180  
 DB 121 GYKSWFAFNSLSTYTRALPVVDDCPPTLGVKQKQPLDSNEIYKLLRRKFFIPDPGS 180  
 QY 181 NMFAFPAQHTHOFPTDHRGPAFTNGLGAGVLIHNYGETLARBQRKLFPGDGKMKY 240  
 DB 181 NMFAFPAQHTHOFPTDHRGPAFTNGLGAGVLIHNYGETLARBQRKLFPGDGKMKY 240  
 QY 241 QIIDGEMYPPTVKTOEMTYPPOVPEHLRPAVQEVFGLVGLMMVATILREHNRVCD 300  
 DB 241 QIIDGEMYPPTVKTOEMTYPPOVPEHLRPAVQEVFGLVGLMMVATILREHNRVCD 300  
 QY 301 VLKQHEHWEGBEQLFOTSRILLGETIKIYIEDVQHLSCGHFLKATDPELLFNKQFOYQ 360  
 DB 301 VLKQHEHWEGBEQLFOTSRILLGETIKIYIEDVQHLSCGHFLKATDPELLFNKQFOYQ 360  
 QY 361 NR1AEPNTLYHMHPLPDTFQIHDQKYNQOFTYNNSSILLEGITQFVSEFTMOIGRV 420  
 DB 361 NR1AEPNTLYHMHPLPDTFQIHDQKYNQOFTYNNSSILLEGITQFVSEFTMOIGRV 420  
 QY 421 AGGRNVPVAVQXVSQASIDSRQMKYQSFNEYRKRFLKPYESFEBELTGKMSAELEAL 480  
 DB 421 AGGRNVPVAVQXVSQASIDSRQMKYQSFNEYRKRFLKPYESFEBELTGKMSAELEAL 480  
 QY 481 YGDIIDAVELYPALLVKEPRPDATFGETMVEVGAPEFLKGLMGVITCSPAWKSTGGEV 540  
 DB 481 YGDIIDAVELYPALLVKEPRPDATFGETMVEVGAPEFLKGLMGVITCSPAWKSTGGEV 540  
 QY 541 GFQIINTVASTIQLICNNVKGCPPTSFVDPDEELIKTYVTINASSRSGLDINFTVLKER 600  
 DB 541 GFQIINTVASTIQLICNNVKGCPPTSFVDPDEELIKTYVTINASSRSGLDINFTVLKER 600  
 QY 601 STEL 604  
 DB 601 STEL 604  
 RESULT 4  
 ID ABB65138 standard; protein; 604 AA.  
 AC ABB65138;  
 XX 12-NOV-2002 (first entry)  
 DE Hypoxia-regulated protein #12.  
 XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
 KW antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;  
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KW preclampsia; atherosclerosis; inflammatory condition; wound healing;  
 XX inflammation; erythropoiesis; hair loss; human.  
 XX OS Homo sapiens.  
 XX MO200246465-A2.  
 PD 13-JUN-2002.  
 XX 10-DEC-2001; 2001WO-GB005458.  
 XX 08-DEC-2000; 2000GB-00030076.  
 PR 08-FEB-2001; 2001GB-00003156.  
 PR 25-OCT-2001; 2001GB-00025666.  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 PA White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
 PI Rayner WN;  
 XX WPI; 2002-627238/67.





QY 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVDLNHIYGETLAROKRLRFKDGKMKY 240  
 Db 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVDLNHIYGETLAROKRLRFKDGKMKY 240  
 QY 241 QIIDGEMYPPTVKDQAEMTYPPQVPEHLRFPAVQGEVFGVGLMMYATIMLEHNRVCD 300  
 Db 241 QIIDGEMYPPTVKDQAEMTYPPQVPEHLRFPAVQGEVFGVGLMMYATIMLEHNRVCD 300  
 QY 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360  
 Db 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360  
 QY 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTROIAGRY 420  
 Db 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTROIAGRY 420  
 QY 421 AGGRNVPAPVQKVSQASIDSRQMKYOSFNEYRRKRFMLKYESFEELTGKEMSALEAL 480  
 Db 421 AGGRNVPAPVQKVSQASIDSRQMKYOSFNEYRRKRFMLKYESFEELTGKEMSALEAL 480  
 QY 481 YGDIADAVELYPALLVEKPRPDALFGETMVEVGAPFSLKGLMGVNICSPAYWKPTFGGEV 540  
 Db 481 YGDIADAVELYPALLVEKPRPDALFGETMVEVGAPFSLKGLMGVNICSPAYWKPTFGGEV 540  
 QY 541 GFQIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRGLDDINPTVLKER 600  
 Db 541 GFQIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRGLDDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

## RESULT 6

ABU03521  
 ID ABU03521 standard; protein; 604 AA.

AC ABU03521;

DT 21-JAN-2003 (first entry)

DE Angiogenesis-associated human protein sequence #66.

KM Human: angiogenesis-associated transcript; angiogenesis;  
 angio genesis-associated disease; cancer; cytostatic.

OS Homo sapiens.

PN W0200279492-A2.

PD 10-OCT-2002.

PF 14-FEB-2002; 2002WO-US004915.

PR 14-FEB-2001; 2001US-00784356.

PR 22-FEB-2001; 2001US-00791390.

PR 19-APR-2001; 2001US-0285475P.

PR 03-AUG-2001; 2001US-0310025P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334244P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PI Murray R, Glynn R, Watson SR, Aziz N;

DR WPI; 2003-040681/03.

DR N-PSDB; ABX08805.

XX

PT Detecting angiogenesis-associated transcript in a cell for diagnosing and  
 PT treating cancer by contacting a sample with a polynucleotide that  
 PT exhibits changes in expression level as a function of time in tissue  
 XX undergoing angiogenesis.

PS Example 2; Page 243; 291pp; English.  
 CC The present invention relates to methods and compositions for detecting  
 CC an angiogenesis-associated transcript in a cell in a patient. The method  
 CC involves contacting a biological sample from the patient with a  
 CC polynucleotide that selectively hybridizes to a sequence at least 80%  
 CC identical to any of the angiogenesis-associated human polynucleotide  
 CC sequences given in the specification. These angiogenesis-associated  
 CC polynucleotide sequences comprise genes that exhibit changes in  
 CC expression levels as a function of time in tissue undergoing  
 CC angiogenesis. The method and the polynucleotide sequences of the  
 CC invention are useful for diagnosing and treating angiogenesis and  
 CC angiogenesis-associated diseases e.g. cancer. The polynucleotide  
 CC sequences are also useful in the gene therapy of such disorders. The  
 CC angiogenesis-associated proteins encoded by the polynucleotide sequences  
 CC are useful as a vaccine for therapeutic and prophylactic immunisation.  
 CC ABU03521-ABU03569 represent angiogenesis-associated protein sequences  
 XX

SQ Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 6; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-300;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLCAVALSHSTANPCSHQONRGVCMVGFQYKDCCTRTGYGNCSTPEEL 60

Db 1 MLARALLCAVALSHSTANPCSHQONRGVCMVGFQYKDCCTRTGYGNCSTPEEL 60

QY 61 TRIKLFLKPTNTVHYIILTHFKGFNNVNNIIPFLNNAISYVLTSSHLIDSPTNYAY 120

Db 61 TRIKLFLKPTNTVHYIILTHFKGFNNVNNIIPFLNNAISYVLTSSHLIDSPTNYAY 120

QY 121 GYKSWAENSNSYTRALPVPVDDCPTPLGVYKQKQLPDSNIVEKLLRRKFIIDPQGS 180

Db 121 GYKSWAENSNSYTRALPVPVDDCPTPLGVYKQKQLPDSNIVEKLLRRKFIIDPQGS 180

QY 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVDLNHIYGETLAROKRLRFKDGKMKY 240

Db 181 NMFAFFAOFHTHOFKTDHKGPAFTNGIGHGVDLNHIYGETLAROKRLRFKDGKMKY 240

QY 241 QIIDGEMYPPTVKDQAEMTYPPQVPEHLRFPAVQGEVFGVGLMMYATIMLEHNRVCD 300

Db 241 QIIDGEMYPPTVKDQAEMTYPPQVPEHLRFPAVQGEVFGVGLMMYATIMLEHNRVCD 300

QY 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360

Db 301 VLKQEHPEWGEOLFOFTRSLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360

QY 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTROIAGRY 420

Db 361 NRIAAEFNTLYHMHPLPDTFOIHDOKYNOQFIYNNSTLLEHGITQVSEFTROIAGRY 420

QY 421 AGGRNVPAPVQKVSQASIDSRQMKYOSFNEYRRKRFMLKYESFEELTGKEMSALEAL 480

Db 421 AGGRNVPAPVQKVSQASIDSRQMKYOSFNEYRRKRFMLKYESFEELTGKEMSALEAL 480

QY 481 YGDIADAVELYPALLVEKPRPDALFGETMVEVGAPFSLKGLMGVNICSPAYWKPTFGGEV 540

Db 481 YGDIADAVELYPALLVEKPRPDALFGETMVEVGAPFSLKGLMGVNICSPAYWKPTFGGEV 540

QY 541 GFQIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRGLDDINPTVLKER 600

Db 541 GFQIINTASIOSLICNNVKGCPFTSFVDPDELIKVTITNASSRGLDDINPTVLKER 600

QY 601 STEL 604

Db 601 STEL 604

XX

RESULT 7  
 ID ABR42250 standard; protein; 604 AA.

AC ABR42250;  
 XX 28-JUL-2003 (first entry)  
 XX Human cyclooxygenase 2 (COX-2).  
 DE Human cyclooxygenase 2 (COX-2).  
 XX Cyclooxygenase 2; COX-2; human; enzyme; vulnerable; osteopathic;  
 KM gene therapy.  
 XX Homo sapiens.  
 OS MO2003022222-2.  
 XX 20-MAR-2003.  
 PD 11-SEP-2002; 2002MO-US028930.  
 XX 11-SEP-2001; 2001US-00953067.  
 XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 PA O'Connor PJ;  
 XX WPI: 2003-313185/30.  
 DR N-PSDB; ACC57774.  
 XX Novel vector useful for enhancing wound healing or treating osteoporosis,  
 PT osteogenesis imperfecta, and brittle bone conditions, comprises a  
 PT promoter linked to a cyclooxygenase expression cassette.  
 XX Disclosure; Page 74-76; 88pp; English.  
 PS The present sequence is the protein sequence of human cyclooxygenase 2  
 CC (COX-2). A claimed vector for use in enhancing wound healing comprises a  
 CC promoter linked to a COX expression cassette, especially encoding a COX-2  
 CC gene product. The vector is used in claimed methods for enhancing wound  
 CC healing and for enhancing wound healing following orthopaedic procedures.  
 CC A claimed method for treating pathological heterotopic ossification,  
 CC especially fibrodysplasia ossificans progressiva, following hip  
 CC replacement or acetabular fracture, involves administering COX-2-  
 CC selective non-steroidal antiinflammatory (NSAID) drugs. The vector is  
 CC also used in a claimed method for treating osteoporosis, osteogenesis  
 CC imperfecta and brittle bone conditions. A claimed composition for use in  
 CC wound healing comprises COX-1, COX-2 or both  
 CC Sequence 604 AA;  
 SQ  
 Query Match 100.0%; Score 3237; DB 6; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-300;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 VLKQEHPEWGDQOLFQTSRLILIGETIKIVIEDYVQHLGSHFKLKPDELLFNKQFOYQ 360  
 QY NRIAEPNTLYHMHPLPDTFOIHDQKXNYOQFIYNNLSILHEGITQFVESFTQIAGRV 420  
 DB 361 NRIAEPNTLYHMHPLPDTFOIHDQKXNYOQFIYNNLSILHEGITQFVESFTQIAGRV 420  
 QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNERYKRFMLKPYESFELTGEKMSALEAL 480  
 DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYQSFNERYKRFMLKPYESFELTGEKMSALEAL 480  
 QY 481 YGDDIVAVELLYPALLYEKRPDAIPEGTEWVGAPSLKGMGNVCSPAYMKPSTFGGEV 540  
 DB 481 YGDDIVAVELLYPALLYEKRPDAIPEGTEWVGAPSLKGMGNVCSPAYMKPSTFGGEV 540  
 QY 541 GFQIINTASISGLICNNYKGCPTSFSPVDPPELLIKVTINASSRSGLDDINPTVLLKER 600  
 DB 541 GFQIINTASISGLICNNYKGCPTSFSPVDPPELLIKVTINASSRSGLDDINPTVLLKER 600  
 QY 601 STEL 604  
 DB 601 STEL 604

RESULT 8  
 ADA20299  
 ID ADA20299 standard; protein; 604 AA.  
 XX  
 AC ADA20299;  
 XX 20-NOV-2003 (first entry)  
 DT Human cyclooxygenase 2 (COX-2) protein wild-type sequence.  
 DE  
 XX Cyclooxygenase 2 gene; COX 2 gene; human; arachidonic acid;  
 XX prostaglandin; Pg; homeostatic function; inflammatory response;  
 KM blood clotting; ovulation; bone metabolism; nerve growth; wound healing;  
 KM immune response; fever; arthritis; Alzheimer's disease; osteoarthritis;  
 KM bone inflammatory condition; cancer; breast cancer; COX-2 modulation;  
 KM clinical response; therapeutic compound; therapeutic dose;  
 XX COX-2 mediated disease; SNP; single nucleotide polymorphism; enzyme.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT 1  
 FT Misc-difference  
 FT /note="This residue can be substituted for an isoleucine  
 FT as a result of a single nucleotide polymorphism"  
 FT Misc-difference 275  
 FT /note="This residue can be substituted for an histidine  
 FT as a result of a single nucleotide polymorphism; This  
 FT possible substitution is at position 275 and not 257 as  
 FT stated in table 3 of the specification"  
 FT Misc-difference 511  
 FT /note="This residue can be substituted for an alanine as  
 FT a result of a single nucleotide polymorphism"  
 XX  
 XX US2003082550-A1.  
 XX  
 XX 01-MAY-2003.  
 XX  
 XX 07-SEP-2001; 2001US-00949293.  
 XX  
 XX 08-SEP-2000; 2000US-0231250P.  
 XX  
 XX (THOM/) THOMANN H.  
 PA (DIAM/) DIAMOND K W.  
 PA (FITZ/) FITZGERALD M G.  
 XX  
 XX Thomann H, Diamond KW, Fitzgerald MG;  
 PI WPI: 2003-596957/56.  
 DR N-PSDB; ADA20274.  
 XX

PT Novel polymorphic sites in cox-2 gene, useful for determining the  
PT therapeutic dose of a compound in the treatment of a cox-2 mediated  
PT disease.

XX Example 1; Fig 4; 23pp; English.

XX This invention relates to a novel isolated nucleic acid, including  
CC polymorphic sites (single nucleotide polymorphism; SNP), which is the  
CC human cyclooxygenase (COX) 2 gene. COX is the key enzyme involved in the  
CC conversion of arachidonic acid to prostaglandins (PGs). PGs are involved  
CC in homeostatic functions as well as inflammatory responses. Some of the  
CC functions of PGs include blood clotting, ovulation, bone metabolism, with  
CC nerve growth, wound healing and immune responses. COX is associated with  
CC various diseases, including fever, arthritis, Alzheimer's disease,  
CC osteoarthritis and other bone inflammatory conditions. COX has also been  
CC shown to be involved in cancer, in particular breast cancer. COX-2  
CC modulation may be useful in the treatment of any of these disorders. The  
CC DNA and protein sequences, including polymorphisms, of the invention may  
CC be useful for predicting the clinical response to a therapeutic compound,  
CC for determining the therapeutic dose of a compound in the treatment of a  
CC COX-2 mediated disease, and for assessing the predisposition of an  
CC individual to diseases mediated by COX-2. The present sequence is that of  
CC the human COX-2 protein, encoded by the gene in which the polymorphic  
CC sites (SNPs) of the invention were identified.

XX Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 7; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1.6e-300;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAALLCAVLAALSHANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEFL 60
DB 1 MAAALLCAVLAALSHANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEFL 60
QY 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPFLRNAMSIVLTSSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPFLRNAMSIVLTSSHLIDSPPTYNADY 120
QY 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPFLRNAMSIVLTSSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPFLRNAMSIVLTSSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSLTYTRALPVPDDCTPLGVKSKKOLPDSNEIVEGLLRKRFIPDQSS 180
DB 121 GYKSWFAFNSLTYTRALPVPDDCTPLGVKSKKOLPDSNEIVEGLLRKRFIPDQSS 180
QY 181 NMWFAFPQHFTHQFKDHRKGPATNGLGAVDLNHYGTLARORRLRFLKQKQKMY 240
DB 181 NMWFAFPQHFTHQFKDHRKGPATNGLGAVDLNHYGTLARORRLRFLKQKQKMY 240
QY 241 QIIDGEMYPPTVKDQOAEWITPPOVBEHLRFVAVGSEVRELVGIMVATWLRHNRYCD 300
DB 241 QIIDGEMYPPTVKDQOAEWITPPOVBEHLRFVAVGSEVRELVGIMVATWLRHNRYCD 300
QY 301 VLKQHPHMGDEOLFQTSRLIIGETIKIVIEDVYQHLSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHMGDEOLFQTSRLIIGETIKIVIEDVYQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAEFTLVHMHLLPDTFOIHQKXNYOQFIYNNISILBHGITQVESFTROIAGRV 420
DB 361 NRIAEFTLVHMHLLPDTFOIHQKXNYOQFIYNNISILBHGITQVESFTROIAGRV 420
QY 421 AGGRNVPAVQKVSQASIDSRQMKYQSFNEFRKRFMLKPYESPPELLGKEMSELEAL 480
DB 421 AGGRNVPAVQKVSQASIDSRQMKYQSFNEFRKRFMLKPYESPPELLGKEMSELEAL 480
QY 481 YGDIIDAVELVALLVEKRPDPAIFGETVNEVGAPSLKGLMGVNI CSPAYMKPSTFGGEV 540
DB 481 YGDIIDAVELVALLVEKRPDPAIFGETVNEVGAPSLKGLMGVNI CSPAYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLCONNVKGCPTSFVSPDELLIKTYVINTASSRSGLDINPTVLKER 600
DB 541 GFOIINTASIOSLCONNVKGCPTSFVSPDELLIKTYVINTASSRSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

DB 601 STEL 604

RESULT 9  
ABM78951

ID ABM78951 standard; protein; 604 AA.

AC ABM78951;

DT 15-JAN-2004 (first entry)

XX Breast cancer specific marker under-expressed in breast cancer.

KW Breast cancer; marker; prostaglandin endoperoxide synthase 2; enzyme;

KX human; diagnosis; cytosolic; biochip; vaccine.

OS Homo sapiens.

PN MO2003073911-A2.

PD 12-SEP-2003.

PF 27-FEB-2003; 2003MO-US005984.

PR 28-FEB-2002; 2002US-0359999P.

PA (GEOU) UNIV GEORGETOWN.

PI Su YA, Yang J;

DR MPI; 2003-721995/68.

DR N-PSDB; ACF79931.

PT Detecting breast cancer in a subject comprises contacting a biological

PT sample with an agent that binds to a polynucleotide or polypeptide of a

PT breast-cancer specific gene (BCSG).

PS Claim 1; Page 121-123; 143pp; English.

XX The present sequence is that of a breast cancer specific marker (BCSM)  
CC encoded by a gene identified by microarray gene expression analysis as  
CC being under-expressed in breast cancers in comparison to healthy tissue.  
CC The BCSM was identified as prostaglandin endoperoxide synthase 2 (PTGS2).  
CC This was previously reported to be undetectable in ductal carcinomas in situ.  
CC Carcinomas and was more likely detected in ductal carcinomas in situ.  
CC PTGS2 was down-regulated in all 13 breast cancer cell lines/tissues  
CC examined. It is 1 of 19 (see ABM78941-59) BCSMs of the invention that are  
CC encoded by breast cancer specific genes (BCSGs) which are differentially  
CC expressed in breast cancer cell lines and breast cancer tissue samples as  
CC compared to control cell lines and normal tissue samples. The invention  
CC provides a method for detection of breast cancer by measuring expression  
CC levels of BCSGs, and in particular the level of polynucleotides  
CC transcribed from and polypeptides encoded by the BCSGs. A pharmaceutical  
CC composition for the treatment of breast cancer comprises a BCSM, an  
CC antibody directed against a BCSM, a vaccine generated using a BCSM, or an  
CC agent that modulates an expression level of a BCSG or an activity of a  
CC BCSM. A biochip for diagnosing breast cancer or screening agents that  
CC inhibit breast cancer comprises a BCSG or BCSM

XX Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 7; Length 604;  
Best Local Similarity 100.0%; Pred. No. 1.6e-300;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAALLCAVLAALSHANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEFL 60
DB 1 MAAALLCAVLAALSHANPCCHPCONRGVMSVGFDOYKDCCTRTGFGENCSPTPEFL 60
QY 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPFLRNAMSIVLTSSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFGKGFVNVNNIPFLRNAMSIVLTSSHLIDSPPTYNADY 120

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QY 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIIDPQGS 180
QY 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRLFKDGKMKY 240
DB 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRLFKDGKMKY 240
QY 241 QITIDGEMVPTVKDQAEIMYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
DB 241 QITIDGEMVPTVKDQAEIMYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
QY 301 VIKQEHPEWGDQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360
DB 301 VIKQEHPEWGDQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360
QY 361 NRIAAEFNLVYHHPPLPDTFQIHDKQKYNQCFIYNNSSILLEGITQFVESFTROLAGRY 420
DB 361 NRIAAEFNLVYHHPPLPDTFQIHDKQKYNQCFIYNNSSILLEGITQFVESFTROLAGRY 420
QY 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNEYRKRKRMKPYESFEELTGKEMSALEAL 480
DB 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNEYRKRKRMKPYESFEELTGKEMSALEAL 480
QY 481 YGDIIDAVELYPALVKEKRPDAIFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
DB 481 YGDIIDAVELYPALVKEKRPDAIFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
QY 541 GFOIINTASTQSLICNNVKGCPFTSFVDPBELIKVTYINASSRSGLDINFTVLKER 600
DB 541 GFOIINTASTQSLICNNVKGCPFTSFVDPBELIKVTYINASSRSGLDINFTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

RESULT 10  
ADD27955

ID ADD27955 standard; protein; 604 AA.

XX ADD27955;

XX 15-JAN-2004 (first entry)

XX Human COX-2 amino acid sequence.

XX Cyclooxygenase type 1; cyclooxygenase type 1 variant protein;

XX COX-1 variant protein; genetic disease; tissue typing;

XX forensic identification; COX-2.

XX Homo sapiens.

XX WO2003029411-A2.

XX 10-APR-2003.

XX 28-SEP-2002; 2002WO-US030947.

XX 28-SEP-2001; 2001US-0326133P.

XX 15-APR-2002; 2002US-0373225P.

XX 16-APR-2002; 2002US-0373661P.

XX 16-SEP-2002; 2002US-0411575P.

XX (UYYO ) UNIV BRIGHAM YOUNG.

XX Simmons D, Chandrasekharan VN;

XX WPI; 2003-421222/39.

XX Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide  
PT encoding the polypeptide, useful for identifying a compound that binds to  
PT and modulates the activity of COX-1 variant polypeptide.

XX Disclosure; Fig 1A; 150pp; English.  
XX  
XX The present invention describes an isolated cyclooxygenase type 1 (COX-1)  
CC variant polypeptide (I). (I) is useful for identifying a compound which  
CC modulates the activity of (I). A nucleotide sequence encoding (I) can be  
CC used for mapping their respective genes on a chromosome, and so locating  
CC gene regions associated with genetic disease, identifying an individual  
CC from a minute biological sample (tissue typing), and to aid in forensic  
CC identification of a biological sample. The present sequence represents a  
CC identification which is used in the exemplification of the present invention.  
XX

Sequence 604 AA;

Query Match 100.0%; Score 3237; DB 7; Length 604;

Best Local Similarity 100.0%; Pred. No. 1,66-300; Indels 0; Gaps 0;

Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLARALLCAVALASHTANPCCSHPQONRGVCMVGFQDKCDCTRTGYGNCSTPEFL 60
DB 1 MLARALLCAVALASHTANPCCSHPQONRGVCMVGFQDKCDCTRTGYGNCSTPEFL 60
QY 61 TRIKFLKPTPTVHYHILTHFKGFNNVYNNIPFLRAIMSYLTSRSHLIDSPPTNADY 120
DB 61 TRIKFLKPTPTVHYHILTHFKGFNNVYNNIPFLRAIMSYLTSRSHLIDSPPTNADY 120
QY 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIIDPQGS 180
QY 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRLFKDGKMKY 240
DB 181 NMWFAFPAQHFTHQFKTDHKGPAFTNGLGHVLDNHYGETLARQRKLRLFKDGKMKY 240
QY 241 QITIDGEMVPTVKDQAEIMYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
DB 241 QITIDGEMVPTVKDQAEIMYPPQVEHLRFVAGQEVFGLVPGMMYATITWLRHNRCVD 300
QY 301 VIKQEHPEWGDQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360
DB 301 VIKQEHPEWGDQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKEPDELLFNKQFOYQ 360
QY 361 NRIAAEFNLVYHHPPLPDTFQIHDKQKYNQCFIYNNSSILLEGITQFVESFTROLAGRY 420
DB 361 NRIAAEFNLVYHHPPLPDTFQIHDKQKYNQCFIYNNSSILLEGITQFVESFTROLAGRY 420
QY 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNEYRKRKRMKPYESFEELTGKEMSALEAL 480
DB 421 AGGRNVPVAVQKVSQASIDQSRQMKYQSFNEYRKRKRMKPYESFEELTGKEMSALEAL 480
QY 481 YGDIIDAVELYPALVKEKRPDAIFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
DB 481 YGDIIDAVELYPALVKEKRPDAIFGETMVEVGAPFSLKGLMGVYICSPAYWKSTFGGEV 540
QY 541 GFOIINTASTQSLICNNVKGCPFTSFVDPBELIKVTYINASSRSGLDINFTVLKER 600
DB 541 GFOIINTASTQSLICNNVKGCPFTSFVDPBELIKVTYINASSRSGLDINFTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

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RESULT 11

ID AAM12698 standard; protein; 604 AA.

XX AAM12698;

XX 04-MAY-1997 (first entry)

XX Human prostaglandin H synthase-2.

KW prostaglandin H synthase-2; PGHS-2; cyclooxygenase; inflammation;  
 KW pulmonary fibrosis; Alzheimer's disease; stroke; acute head injury;  
 KW endometriosis; dysmenorrhea; pre-term labour; prostate cancer;  
 KW colorectal cancer; squamous cell carcinoma; breast cancer;  
 KW oral pharyngeal cancer; stomach cancer; fibrosarcoma; skin cancer;  
 KW osteosarcoma; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 PN WO6640720-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 03-JUN-1996; 96WO-US008311.  
 XX  
 PR 07-JUN-1995; 95US-00487752.  
 XX  
 PA (UVRP) UNITV ROCHESTER.  
 XX  
 PI Young DA, O'bannon MK, Winn VD;  
 XX  
 DR MPI: 1997-052220/05.  
 XX N-PSDB; AAT59635.  
 PT Nucleic acid encoding human prostaglandin H synthase-2 - used in treating  
 PT and detection of inflammation, pre-term labour, cancer, etc.  
 XX  
 PS Example 9; Page 84-85; 126pp; English.  
 XX  
 CC Human prostaglandin H synthase 2 (PGHS-2) (AA012698) is responsible for  
 CC increased prostaglandin synthesis associated with inflammation. Unlike  
 CC PGHS-1, expression of PGHS-2 is responsive to regulatory control. The  
 CC PGHS-2 amino acid sequence was deduced from a DNA clone (AAT59635)  
 CC isolated from human fibroblast W138 cells. Transfected host cells  
 CC expressing human PGHS-2 can be used to identify cpts. that modulate PGHS-  
 CC 2 expression and activity. Cpts. that inhibit expression may be used to  
 CC treat inflammation, e.g. arterial inflammation or pulmonary fibrosis,  
 CC Alzheimer's disease, stroke, acute head injury, endometriosis,  
 CC dysmenorrhea, pre-term labour, cancer and radiation-induced injury.  
 CC Antibodies immunospecific PGHS-2 may be used to detect PGHS-2 expression,  
 CC and thus in diagnosis of certain cancers  
 CC  
 XX Sequence 604 AA;  
 SQ  
 Query Match 99.9%; Score 3234; DB 2; Length 604;  
 Best Local Similarity 99.8%; Pred. No. 3.1e-300;  
 Matches 603; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 361 NR1AAEFNTLYHMHLPDFTFQIHDQKXNYQOFTYNSILLEGITQFVSFTRQIAGRV 420  
 QY 421 AGGRNVPVAVQXVSQASIDSRQMYQSFNEYKRFPMILKYESFEELTGKENSALFEAL 480  
 DB 421 AGGRNVPVAVQXVSQASIDSRQMYQSFNEYKRFPMILKYESFEELTGKENSALFEAL 480  
 QY 481 YGDIIDAVELPALVKEPRDAIFGETMVEVGAFFSLKGLMGVYCSPAYWKPESTFGGEV 540  
 DB 481 YGDIIDAVELPALVKEPRDAIFGETMVEVGAFFSLKGLMGVYCSPAYWKPESTFGGEV 540  
 QY 541 GFQIINTASIQSLICNNVKGCPFTSFPVPELILKTYTINASSSRGLDINPTVLKER 600  
 DB 541 GFQIINTASIQSLICNNVKGCPFTSFPVPELILKTYTINASSSRGLDINPTVLKER 600  
 QY 601 STEL 604  
 DB 601 STEL 604

RESULT 12  
 AARS1267  
 ID AARS1267 standard; protein; 604 AA.  
 XX  
 AC AARS1267;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-OCT-1994 (first entry)

DE Sequence of human prostaglandin G/H synthase-2 (PGHS-2).  
 XX  
 KW Prostaglandin; hormone; eicosanoid; fatty acid metabolism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9406919-A2.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 22-SEP-1993; 93WO-US009167.  
 XX  
 PR 22-SEP-1992; 92US-00949780.  
 PR 01-DEC-1992; 92US-00983835.  
 PR 22-MAR-1993; 93US-00034143.  
 PR 28-APR-1993; 93US-00054364.  
 XX  
 PA (UVRP) UNITV ROCHESTER.  
 XX  
 PI Young DA, O'bannon MK, Winn VD;  
 XX  
 DR MPI: 1994-118468/14.  
 XX N-PSDB; AA061790.  
 PT New prostaglandin G/H synthase-2 gene - used for producing transgenic  
 PT cell lines for testing ability of cpts. to inhibit synthesis of  
 PT prostaglandin(s).  
 XX  
 PS Claim 40; Page 45-47; 76pp; English.  
 XX  
 CC RNA was isolated from a human fibroblast cell line (W138). PCR primers  
 CC specific for the human PGHS-1 and PGHS-2 sequences were engineered to  
 CC amplify the coding regions of either one transcript or the other (see  
 CC AA061792-95). PCR products of about 2 kb were generated. Three PGHS-2  
 CC clones were sequenced in both directions. The clone comprising the PGHS-2  
 CC sequence disclosed in AA061790 was selected for transfection. This  
 CC sequence differs from the human PGHS-2 sequence disclosed by Hla and  
 CC Hellson, PNAS, 89, 7384 (1992) due to a Glu rather than a Gly at AA posn.  
 CC 165. Mouse PGHS-2 also has a Glu at this posn. (Updated on 25-MAR-2003 to  
 CC correct FN field.) (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 XX Sequence 604 AA;  
 SQ

Query Match 97.0%; Score 3140; DB 2; Length 604;



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Db          541 KGCFSTSFVDP 553
|||||
RESULT 14
ID ABB07248 standard; protein; 604 AA.
XX
AC ABB07248;
XX
DT 26-MAR-2002 (first entry)
XX
DE Rabbit cyclooxygenase-2 (COX-2) protein.
XX
KW Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;
XX inflammation; central nervous system; rabbit.
OS Oryctolagus cuniculus.
XX
PN M020011026-A1.
XX
PD 15-FEB-2001.
XX
PF 04-AUG-2000; 2000MO-US019565.
XX
PR 06-AUG-1999; 99US-0147601P.
XX
PA (SEAR ) SEARLE & CO G D.
XX
PI Gierse JK;
XX
DR WPI; 2002-113777/15.
XX
PT Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful
XX for identifying drugs that can reduce inflammation in dogs, and screening
XX selective inhibitors of cyclooxygenase-2 protein.
XX
PS Disclosure; Fig 3; 122pp; English.
XX
CC The invention relates to genes that encode canine cyclooxygenase (COX)-1
CC or COX-2 proteins. The COX proteins, especially COX-2 is useful for
CC diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its
CC fragment is useful for identifying a test material which has the ability
CC to inhibit, suppress, modulate, or maintain canine COX-2 activity. The
CC COX-1 and COX-2 polynucleotides are useful for determining an association
CC between a polymorphism and a trait. COX-2 cDNA molecules and methods
CC provided are also useful for diagnosing or prognosing an association
CC condition such as arthritis, cancer, neoplasia, inflammation or central
CC nervous system disorder in a dog. The present sequence represents a
CC rabbit COX-2 protein, used in comparison studies with the canine COX-2
XX
SQ Sequence 604 AA:
Query Match          91.8%; Score 2971; DB 5; Length 604;
Best Local Similarity 89.9%; Pred. No. 4.8e-275;
Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;
QY 1 MLARALLCAVALSHANPCCHPCNRCVCMVGFDQYKCDCTRTGFGENCSPTPEFL 60
Db 1 MLARALLCAVALSHANPCCHPCNRCVCMVGFDQYKCDCTRTGFGENCSPTPEFL 60
QY 61 TRIKLFKPTPTNTVHYLLTHFKGPMNVNIIPLRNAINSYVLTSRSHLIDSPPTYNADY 120
Db 61 TRIKLFKPTPTNTVHYLLTHFKGPMNVNIIPLRNAINSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYSWMAFNSLSYTRALPVPDPCEPTPLGVKGGKOLPDSNETVEKLLRRKRTIPPOGS 180
Db 121 GYSWMAFNSLSYTRALPVPDPCEPTPLGVKGGKOLPDSNETVEKLLRRKRTIPPOGS 180
QY 122 NYKSWMAFNSLSYTRALPVPADCPPTMGVKKKEIPDSKDVVEKLLRRKRTIPPOG 180
Db 122 NYKSWMAFNSLSYTRALPVPADCPPTMGVKKKEIPDSKDVVEKLLRRKRTIPPOG 180
QY 181 NMMAFAFAQHTTQCFKTHKRGPAFTNGIGSHGVNDINHLYGETTLARQRLKLFKDGKMKY 240
Db 181 NMMAFAFAQHTTQCFKTHKRGPAFTNGIGSHGVNDINHLYGETTLARQRLKLFKDGKMKY 240

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QY 241 QIIDGEMRPPTVKDQTOAEMTPPVPEHLRFPAVQEVFGLVPGIMMYATIMREHNRVCD 300
Db 241 QVIDGEVYPPPTVKDQTOEMTPPVPHIPAHQFAVQEVFGLVPGIMMYATIMREHNRVCD 300
QY 301 VLKQEHPEWDEQLFQTSRLILIGETIKTIVIEDYVQHLSCYHNRKLPDELLFNKQFOYQ 360
Db 301 VLKQEHPEWDEQLFQTSRLILIGETIKTIVIEDYVQHLSCYHNRKLPDELLFNKQFOYQ 360
QY 361 NRJAEFNTLYHWHPLPDTFQIHQKYNQCFIYNNISILLEGITQFVSEFTROLAGRV 420
Db 361 NRJAEFNTLYHWHPLPDTFQIHQKYNQCFIYNNISILLEGITQFVSEFTROLAGRV 420
QY 421 AGGRNVPVAVQKASIDQSRMKYQSNREYRKRFMLKPYSEFEELTGKEMASLEAL 480
Db 421 AGGRNVPVAVQKASIDQSRMKYQSNREYRKRFMLKPYSEFEELTGKEMASLEAL 480
QY 481 YGDIDAVELYPALLVKKPRDAIFGRTWEVGAPELKGIMNVITCSPAWKESTGGEV 540
Db 481 YGDIDAVELYPALLVKKPRDAIFGRTWEVGAPELKGIMNVITCSPAWKESTGGEV 540
QY 541 GFQIINTASTQSLICNNVKGCEFTSPSVDPDELIKVTINASSRGLDINDPTVLLKGR 600
Db 541 GFQIINTASTQSLICNNVKGCEFTSPSVDPDELIKVTINASSRGLDINDPTVLLKGR 600
QY 601 STEL 604
Db 601 STEL 604
RESULT 15
ADD27960
ID ADD27960 standard; protein; 604 AA.
XX
AC ADD27960;
XX
DT 15-JAN-2004 (first entry)
XX
DE Rabbit COX-2 amino acid sequence.
XX
KW cyclooxygenase type 1; cyclooxygenase type 1 variant protein;
XX forensic identification; COX-2.
XX
OS Oryctolagus cuniculus.
XX
PN M02003029411-A2.
XX
PD 10-APR-2003.
XX
PF 28-SEP-2002; 2002MO-US030947.
XX
PR 28-SEP-2001; 2001US-0326133P.
XX
PR 15-APR-2002; 2002US-0373225P.
XX
PR 16-APR-2002; 2002US-0373661P.
XX
PR 16-SEP-2002; 2002US-0411575P.
XX
PA (UYYO ) UNIV BRIGHAM YOUNG.
XX
PI Simmons D, Chandrasekharan VN;
XX
DR WPI; 2003-421222/39.
XX
PT Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide
XX encoding the polypeptide, useful for identifying a compound that binds to
XX PT and modulates the activity of COX-1 variant polypeptide.
XX
PS Disclosure; Fig 1A; 150pp; English.
XX
CC The present invention describes an isolated cyclooxygenase type 1 (COX-1)
CC variant polypeptide (I). (I) is useful for identifying a compound which
CC modulates the activity of (I). A nucleotide sequence encoding (I) can be
CC used for mapping their respective genes on a chromosome, and so locating
CC gene regions associated with genetic disease, identifying an individual

```

CC from a minute biological sample (tissue typing), and to aid in forensic  
CC identification of a biological sample. The present sequence represents a  
CC sequence which is used in the exemplification of the present invention.

XX  
SQ Sequence 604 AA;

Query Match 91.8%; Score 2971; DB 7; Length 604;

Best Local Similarity 89.9%; Pred. No. 4.8e-275; Mismatches 26; Indels 0; Gaps 0;

Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;

```
QY 1 MLARALLICAVLALSHSTANPCSSHPCQNRGVMSVGDQYKDCCTRTGYGNCSTBEFL 60
Db 1 MLARALLICAVLALSHSTANPCSSHPCQNRGVMSVGDQYKDCCTRTGYGNCSTBEFL 60
QY 61 TRIKLFKPTNTVHYIITHFKGFWNVNNIPEFLNAINSVLTSRSLIDSPPTYNADY 120
Db 61 TRIKLFKPTNTVHYIITHFKGFWNVNNIPEFLNAINSVLTSRSLIDSPPTYNADY 120
QY 121 GYKSWAASNSIYTRALPVDPDCEPTLVGKKGKOLPDSNEIVEKLLRRKFIPTPOGS 180
Db 121 GYKSWAASNSIYTRALPVDPDCEPTLVGKKGKOLPDSNEIVEKLLRRKFIPTPOGS 180
QY 121 NYKSWAASNSIYTRALPVDPDCEPTLVGKKGKOLPDSNEIVEKLLRRKFIPTPOGS 180
Db 121 NYKSWAASNSIYTRALPVDPDCEPTLVGKKGKOLPDSNEIVEKLLRRKFIPTPOGS 180
QY 181 NMFAFPAQHTHGFTHDHRKPAFTNGLGHVLDNHIYGETLARQRRLFKDGMKY 240
Db 181 NMFAFPAQHTHGFTHDHRKPAFTNGLGHVLDNHIYGETLARQRRLFKDGMKY 240
QY 241 QIIDSEMYPTVKTQAEIYPPQVEHIREAVGQEVGGLVPGIMMYATITWREHNRVCD 300
Db 241 QIIDSEMYPTVKTQAEIYPPQVEHIREAVGQEVGGLVPGIMMYATITWREHNRVCD 300
QY 241 QVIDGEVYPTVKTQAEIYPPQVEHIREAVGQEVGGLVPGIMMYATITWREHNRVCD 300
Db 241 QVIDGEVYPTVKTQAEIYPPQVEHIREAVGQEVGGLVPGIMMYATITWREHNRVCD 300
QY 301 VIKQHPREMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFDPPELLFNKQFOYQ 360
Db 301 VIKQHPREMGDEQLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLFDPPELLFNKQFOYQ 360
QY 361 NRIAEFNTLYMHPLPDPFQIHQKXNYQOFIYNNISILLEGITQFVSEFTROIAGRY 420
Db 361 NRIAEFNTLYMHPLPDPFQIHQKXNYQOFIYNNISILLEGITQFVSEFTROIAGRY 420
QY 421 AGGRNVPPAVQKASIDQSRQMKYQSNERYKRLKPYESFEELTGKEMAELEAL 480
Db 421 AGGRNVPPAVQKASIDQSRQMKYQSNERYKRLKPYESFEELTGKEMAELEAL 480
QY 481 YGIDDAVELYPALVKKPRDALFGEIYVGVGAPFSLKGLMGNVICSPAYMKPSTFGGEV 540
Db 481 YGIDDAVELYPALVKKPRDALFGEIYVGVGAPFSLKGLMGNVICSPAYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFPDPELIKTYTINASSRSGLDINPTVLKER 600
Db 541 GFOIINTASIOSLICNNVKGCPFTSFPDPELIKTYTINASSRSGLDINPTVLKER 600
QY 601 STEL 604
Db 601 STEL 604
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Search completed: April 24, 2004, 07:19:19  
Job time : 81 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 24, 2004, 07:17:00 ; Search time 25 Seconds

(without alignments)  
1247.283 Million cell updates/sec

Title: US-08-064-271-10  
Perfect score: 3237

Sequence: 1 MBLRALLCAVLAHSHTAMP.....RSGLDINPTVLKERSTEL 604

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Issued Patents AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
7: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3237	100.0	604	1	US-08-064-271-10
2	3237	100.0	604	1	US-08-487-753-4
3	3237	100.0	604	2	US-08-480-065-4
4	3237	100.0	604	3	US-08-487-744-4
5	3237	100.0	604	3	US-08-930-589A-18
6	3237	100.0	604	4	US-09-599-781-18
7	3237	100.0	604	5	PCT-US93-09167-4
8	3230	99.8	604	1	US-08-487-753-5
9	3230	99.8	604	2	US-08-480-065-5
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14	2873	88.8	604	2	US-08-480-065-2
15	2873	88.8	604	3	US-08-487-744-2
16	2873	88.8	604	5	PCT-US93-09167-2
17	2029.5	62.7	633	4	US-09-919-060-13
18	885	27.3	180	4	US-09-919-060-2
19	313	9.7	91	4	US-09-919-060-10
20	225	7.0	913	3	US-08-911-853-17
21	225	7.0	913	3	US-09-479-409-17
22	225	7.0	913	4	US-09-479-453-17
23	160.5	5.0	933	2	US-08-313-200-1
24	160.5	5.0	933	4	US-09-251-039-2
25	160.5	5.0	933	5	PCT-US93-03837-1
26	160	4.9	1551	4	US-09-437-568A-46
27	149.5	4.6	695	6	5460961-5

28	115	3.6	3135	1	US-08-323-170B-2	Sequence 2, Appli
29	115	3.6	3135	4	US-08-954-441-2	Sequence 2, Appli
30	112	3.5	667	4	US-09-107-532A-3749	Sequence 3749, Ap
31	110.5	3.4	1525	3	US-09-191-647-2	Sequence 2, Appli
32	110.5	3.4	1525	3	US-09-540-245A-2	Sequence 2, Appli
33	110.5	3.4	1525	3	US-09-540-153-2	Sequence 2, Appli
34	109	3.4	2471	1	US-08-185-432-16	Sequence 16, Appli
35	109	3.4	2471	1	US-08-083-590A-19	Sequence 19, Appli
36	109	3.4	2471	3	US-08-532-384-19	Sequence 19, Appli
37	109	3.4	2471	4	US-08-899-232-1	Sequence 1, Appli
38	108.5	3.4	661	1	US-08-375-709-3	Sequence 3, Appli
39	108.5	3.4	1075	1	US-07-623-033-2	Sequence 2, Appli
40	108.5	3.4	2165	1	US-08-514-975B-2	Sequence 2, Appli
41	108.5	3.4	2165	5	PCT-US95-12507-2	Sequence 2, Appli
42	108.5	3.3	1529	4	US-09-112-283C-396	Sequence 396, App
43	107.5	3.3	543	4	US-09-328-352-7396	Sequence 2, Appli
44	107	3.3	559	4	US-09-672-749-2	Sequence 2, Appli
45	107	3.3				

#### ALIGNMENTS

RESULT 1

US-08-064-271-10  
Sequence 10, Application US/08064271

Patent No. 5543297

GENERAL INFORMATION:

APPLICANT: Kennedy, Brian P.

APPLICANT: Cromlish, Wanda A.

APPLICANT: Mancini, Joseph A.

APPLICANT: O'Neill, Gary J.

APPLICANT: Vickers, Philip J.

APPLICANT: Wong, Elizabeth

TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in, 1.4kb

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7

SOFTWARE: Microsoft Word 5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/064,271

FILING DATE: 19930506

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Panzer, Curtis C.

REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 189061A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3199

TELEFAX: (908)594-4720

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0%; Score 3237; DB 1; Length 604;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLICAVIALSHTANPCCSHPCQNRGVMSVGFQYKDCDCTRTGFYGENCSTPEFL 60  
 DB 1 MLARALLICAVIALSHTANPCCSHPCQNRGVMSVGFQYKDCDCTRTGFYGENCSTPEFL 60  
 QY 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120  
 DB 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120  
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 DB 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVYKQKQLPDSNIEVEKLLRRKFIPDPQS 180  
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 DB 181 NMMPFAFQHFTHQFKTDHKGPAFTNGLGHVDLNIYGETLARORRLRFLKQGMKY 240  
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 DB 241 QIIDGEMPTVKDQAEIMTYPPQVEHLRFVGVGEVFLVGLMMYATIMLRHNRYCD 300  
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 DB 301 VKQHEPWEGBOLPQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360  
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 DB 361 NR1AAEFNTLYHWHPLPDTFQIHQKXVQCFYNNNSILLEGITQFVESFTROLAGRY 420  
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 DB 421 AGGRNVPAPVOKVQASIDQSRQMKYQSFNEYKRFMLKYESFEEITGKEKMSAELEAL 480  
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 DB 481 YGDIADVELYPALVKEKRPDAIFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540  
 QY 541 GFOIINTASIOSLICNNVKCPTSFVDPDELIKITYTINASSRSGLDINFTVLKER 600  
 DB 541 GFOIINTASIOSLICNNVKCPTSFVDPDELIKITYTINASSRSGLDINFTVLKER 600  
 QY 601 STEL 604  
 DB 601 STEL 604  
 RESULT 2  
 US-08-487-753-4  
 ; Sequence 4, Application US/08487753  
 ; Patent No. 5807733  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Donald A.  
 ; APPLICANT: O'Banion, Michael K.  
 ; APPLICANT: Winn, Virginia D.  
 ; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2  
 ; TITLE OF INVENTION: FUSION PROTEINS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/487,753  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3996-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELE: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; US-08-487-753-4  
 Query Match 100.0%; Score 3237; DB 1; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLARALLICAVIALSHTANPCCSHPCQNRGVMSVGFQYKDCDCTRTGFYGENCSTPEFL 60  
 DB 1 MLARALLICAVIALSHTANPCCSHPCQNRGVMSVGFQYKDCDCTRTGFYGENCSTPEFL 60  
 QY 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120  
 DB 61 TRIKFLKPTENTVHYILTHEKGFNNVNNIPEFLNALSIVLTSRSHLIDSPPTYNADY 120  
 QY 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVYKQKQLPDSNIEVEKLLRRKFIPDPQS 180  
 DB 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVYKQKQLPDSNIEVEKLLRRKFIPDPQS 180  
 QY 181 NMMPFAFQHFTHQFKTDHKGPAFTNGLGHVDLNIYGETLARORRLRFLKQGMKY 240  
 DB 181 NMMPFAFQHFTHQFKTDHKGPAFTNGLGHVDLNIYGETLARORRLRFLKQGMKY 240  
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 DB 241 QIIDGEMPTVKDQAEIMTYPPQVEHLRFVGVGEVFLVGLMMYATIMLRHNRYCD 300  
 QY 301 VKQHEPWEGBOLPQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360  
 DB 301 VKQHEPWEGBOLPQTSRLIIGETIKIVIEDYVQHSYHFKLKEPDELLFNKQFOYQ 360  
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 DB 361 NR1AAEFNTLYHWHPLPDTFQIHQKXVQCFYNNNSILLEGITQFVESFTROLAGRY 420  
 QY 421 AGGRNVPAPVOKVQASIDQSRQMKYQSFNEYKRFMLKYESFEEITGKEKMSAELEAL 480  
 DB 421 AGGRNVPAPVOKVQASIDQSRQMKYQSFNEYKRFMLKYESFEEITGKEKMSAELEAL 480  
 QY 481 YGDIADVELYPALVKEKRPDAIFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540  
 DB 481 YGDIADVELYPALVKEKRPDAIFGETMVEVGAFFSLKGLMGVITCSPAYWKSTFGGEV 540  
 QY 541 GFOIINTASIOSLICNNVKCPTSFVDPDELIKITYTINASSRSGLDINFTVLKER 600  
 DB 541 GFOIINTASIOSLICNNVKCPTSFVDPDELIKITYTINASSRSGLDINFTVLKER 600  
 QY 601 STEL 604  
 DB 601 STEL 604  
 RESULT 3  
 US-08-480-065-4  
 ; Sequence 4, Application US/08480065  
 ; Patent No. 5837479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Donald A.  
 ; APPLICANT: O'Banion, Michael K.  
 ; APPLICANT: Winn, Virginia D.

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/ TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF
/ TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,065
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 3996-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 604 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-480-065-4

Query Match      100.0%; Score 3237; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLCAVALALSHANPCSHPCONRGVMSVGFPOYKDCDCTRTGFGNGCSTPEFL 60
DB 1 MLARALLCAVALALSHANPCSHPCONRGVMSVGFPOYKDCDCTRTGFGNGCSTPEFL 60
QY 61 TRIKFLKPTPTVHYILTHFKGFNVVNNIPFLNNAIMSYVLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVHYILTHFKGFNVVNNIPFLNNAIMSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDPGGS 180
DB 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDPGGS 180
QY 181 NMFAFAFHQFTHQFETDHRKGPATNGLGHGVLDNHIYGETLARQRKRLFKXGKMKY 240
DB 181 NMFAFAFHQFTHQFETDHRKGPATNGLGHGVLDNHIYGETLARQRKRLFKXGKMKY 240
QY 241 QIIDEMPTPTVKTQAEIMYPPQVEHLRFAVGGEVFGVLVGLMMYATITMLREHNRVCD 300
DB 241 QIIDEMPTPTVKTQAEIMYPPQVEHLRFAVGGEVFGVLVGLMMYATITMLREHNRVCD 300
QY 301 VIKOSHPEMGDEQLQTSRLILIGETIKIVIEDYVQHSGLFKLPDELLFNKQFOYO 360
DB 301 VIKOSHPEMGDEQLQTSRLILIGETIKIVIEDYVQHSGLFKLPDELLFNKQFOYO 360
QY 361 NRIAEFNTLYMHMLDPTFOIHQKXVYQOFIYNNLSLLEHGIQFVSESTRQIAGV 420
DB 361 NRIAEFNTLYMHMLDPTFOIHQKXVYQOFIYNNLSLLEHGIQFVSESTRQIAGV 420
QY 421 AGGRVNPVAVQVQASIDQSFQKMYQSFNEVYRKFPMKPYBSFELTGCEKMSALEAL 480
DB 421 AGGRVNPVAVQVQASIDQSFQKMYQSFNEVYRKFPMKPYBSFELTGCEKMSALEAL 480
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DB 481 YGDIDAVELYPALLVEKRPDAIFGETIWEVGAFFSLKGLMGNVICSPIYKPSFTFGGEV 540
QY 541 GFQIINTASTQSLICNNVKKCPPTSFVSDPELIKVTYINASSRSSGDIINPTVLKER 600
DB 541 GFQIINTASTQSLICNNVKKCPPTSFVSDPELIKVTYINASSRSSGDIINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 4
US-08-487-744-4
/ Sequence 4: Application US/08487744
/ Patent No. 6048850
/ GENERAL INFORMATION:
/ APPLICANT: Young, Donald A.
/ APPLICANT: O'Banion, Michael K.
/ APPLICANT: Winn, Virginia D.
/ TITLE OF INVENTION: METHODS FOR INHIBITING PROSTAGLANDIN
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,744
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 3996-013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 604 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-487-744-4

Query Match      100.0%; Score 3237; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLCAVALALSHANPCSHPCONRGVMSVGFPOYKDCDCTRTGFGNGCSTPEFL 60
DB 1 MLARALLCAVALALSHANPCSHPCONRGVMSVGFPOYKDCDCTRTGFGNGCSTPEFL 60
QY 61 TRIKFLKPTPTVHYILTHFKGFNVVNNIPFLNNAIMSYVLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTPTVHYILTHFKGFNVVNNIPFLNNAIMSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDPGGS 180
DB 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVGKKQLPDSNEIVEKLLRRKFIPDPGGS 180
QY 181 NMFAFAFHQFTHQFETDHRKGPATNGLGHGVLDNHIYGETLARQRKRLFKXGKMKY 240

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Db      181 NMMAFAFAQHFTHQFPTDHRKGPFTNGIGHGVDLNHIYGETLARQKRLFKDGKMKY 240
QY      241 QIIDGEMYPPTVKDQAEMLYPPQVEHLREAVGQVEFGVPGIMMYATITWLRHNRYCD 300
Db      241 QIIDGEMYPPTVKDQAEMLYPPQVEHLREAVGQVEFGVPGIMMYATITWLRHNRYCD 300
QY      301 VLKQEHPEWGEQLFQTSRLILIGETIKIVIEDYVGHLSGYHKLKFPDELLFNKQFOYQ 360
Db      301 VLKQEHPEWGEQLFQTSRLILIGETIKIVIEDYVGHLSGYHKLKFPDELLFNKQFOYQ 360
QY      361 NRIAAEFNTLYHMHPLPDTFQIHDQKXNQCFIYNNSSILLEGITQFVSSFROIAGRY 420
Db      361 NRIAAEFNTLYHMHPLPDTFQIHDQKXNQCFIYNNSSILLEGITQFVSSFROIAGRY 420
QY      421 AGGRNVPAPVQKYSQASIDSRQMKYQFNEYRKRREMLKYESFEEELTGKEMSAELEAL 480
Db      421 AGGRNVPAPVQKYSQASIDSRQMKYQFNEYRKRREMLKYESFEEELTGKEMSAELEAL 480
QY      481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGLMGVTCSPAYWKSTFGGEV 540
Db      481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGLMGVTCSPAYWKSTFGGEV 540
QY      541 GFOIINTASIQSLICNNVKGCPFTSFVDPDELKIVTINASSRSGLDINPTVLKER 600
Db      541 GFOIINTASIQSLICNNVKGCPFTSFVDPDELKIVTINASSRSGLDINPTVLKER 600
QY      601 STEL 604
Db      601 STEL 604

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## RESULT 5

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US-08-930-589A-18
; Sequence 18, Application US/08930589A
; Patent No. 6107087
; GENERAL INFORMATION:
; APPLICANT: MERCK FROST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930.589A
; FILING DATE: 28-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19029PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-589A-18

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Query Match      100.0%; Score 3237; DB 3; Length 604;
Best Local Similarity 100.0%; Pred No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLARALLCAVALASTNAPCCSHPCQNRGVCSVGFQYKDCCTRTGYGENCSTPEEL 60
QY      61 TRIKLFLKPTPTVTHILTHFKGFNVVNNIPFLRNAISYVLTSRSHLIDSPPTNAY 120
Db      61 TRIKLFLKPTPTVTHILTHFKGFNVVNNIPFLRNAISYVLTSRSHLIDSPPTNAY 120
QY      121 GYKSWAFSNLSYTTALPVPDDCPTPLGVKSKQLPDSNETIVEKILLRRKFIIPDQGS 180
Db      121 GYKSWAFSNLSYTTALPVPDDCPTPLGVKSKQLPDSNETIVEKILLRRKFIIPDQGS 180
QY      181 NMMAFAFAQHFTHQFPTDHRKGPFTNGIGHGVDLNHIYGETLARQKRLFKDGKMKY 240
Db      181 NMMAFAFAQHFTHQFPTDHRKGPFTNGIGHGVDLNHIYGETLARQKRLFKDGKMKY 240
QY      241 QIIDGEMYPPTVKDQAEMLYPPQVEHLREAVGQVEFGVPGIMMYATITWLRHNRYCD 300
Db      241 QIIDGEMYPPTVKDQAEMLYPPQVEHLREAVGQVEFGVPGIMMYATITWLRHNRYCD 300
QY      301 VLKQEHPEWGEQLFQTSRLILIGETIKIVIEDYVGHLSGYHKLKFPDELLFNKQFOYQ 360
Db      301 VLKQEHPEWGEQLFQTSRLILIGETIKIVIEDYVGHLSGYHKLKFPDELLFNKQFOYQ 360
QY      361 NRIAAEFNTLYHMHPLPDTFQIHDQKXNQCFIYNNSSILLEGITQFVSSFROIAGRY 420
Db      361 NRIAAEFNTLYHMHPLPDTFQIHDQKXNQCFIYNNSSILLEGITQFVSSFROIAGRY 420
QY      421 AGGRNVPAPVQKYSQASIDSRQMKYQFNEYRKRREMLKYESFEEELTGKEMSAELEAL 480
Db      421 AGGRNVPAPVQKYSQASIDSRQMKYQFNEYRKRREMLKYESFEEELTGKEMSAELEAL 480
QY      481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGLMGVTCSPAYWKSTFGGEV 540
Db      481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGLMGVTCSPAYWKSTFGGEV 540
QY      541 GFOIINTASIQSLICNNVKGCPFTSFVDPDELKIVTINASSRSGLDINPTVLKER 600
Db      541 GFOIINTASIQSLICNNVKGCPFTSFVDPDELKIVTINASSRSGLDINPTVLKER 600
QY      601 STEL 604
Db      601 STEL 604

```

## RESULT 6

```

US-09-599-781-18
; Sequence 18, Application US/09599781
; Patent No. 6362327
; GENERAL INFORMATION:
; APPLICANT: MERCK FROST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,781
FILING DATE: 21-Jun-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,033
FILING DATE: 27-Sep-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coppola, Joseph A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19029PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-599-781-18

Query Match      100.0%; Score 3237; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLICAVLALSHSTANPCSHPCONRGVCMVSGFDYKDCDCTRTGFGNGCSTPEEL 60
DB 1 MLARALLICAVLALSHSTANPCSHPCONRGVCMVSGFDYKDCDCTRTGFGNGCSTPEEL 60
QY 61 TRIKFLKPTNTVHYILTHFKGFNNVNNIPFLRNAINMSYVLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFKGFNNVNNIPFLRNAINMSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAEFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
DB 121 GYKSWAEFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
QY 121 GYKSWAEFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
DB 121 GYKSWAEFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
QY 181 NMMAFAFQHTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFLKGGKMY 240
DB 181 NMMAFAFQHTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFLKGGKMY 240
QY 241 QIIDGEMTPPYVKTQDAEMITPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 300
DB 241 QIIDGEMTPPYVKTQDAEMITPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 300
QY 301 VIKQHPHMGDEQLPQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VIKQHPHMGDEQLPQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAAEFNTLYEMHPLPDTFOIHDQKYNVQOFTYNNSTLLEHGITQFVESFTROIAGRV 420
DB 361 NRIAAEFNTLYEMHPLPDTFOIHDQKYNVQOFTYNNSTLLEHGITQFVESFTROIAGRV 420
QY 421 AGGRVVPRAVQVQASIDQSFOMKYQSFENEYRKRFMLKPYSPFELTGEKEMSALEEL 480
DB 421 AGGRVVPRAVQVQASIDQSFOMKYQSFENEYRKRFMLKPYSPFELTGEKEMSALEEL 480
QY 481 YGDIIDAVELYPALILEKRPDAIFGETMVEVAPPSLGLMGWNYCSPAYWKPSTFGGEV 540
DB 481 YGDIIDAVELYPALILEKRPDAIFGETMVEVAPPSLGLMGWNYCSPAYWKPSTFGGEV 540
QY 541 GFOIINTASIGSLICNNVKGCPFTSFVDDPELLIKTVITINASSSSGDDINPTVLLKER 600
DB 541 GFOIINTASIGSLICNNVKGCPFTSFVDDPELLIKTVITINASSSSGDDINPTVLLKER 600

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QY 601 STEEL 604
DB 601 STEEL 604

RESULT 7
PCT-US93-09167-4
Sequence 4, Application PC/TUS9309167
GENERAL INFORMATION:
APPLICANT: Young, Donald A.
APPLICANT: O'Banion, M. Kerry
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: Stably-Transformed Mammalian Cells
TITLE OF INVENTION: Expressing a Regulated, Inflammatory Cyclooxygenase
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Norwest Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 8840.20-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Amino acid sequence for Human PGHS-2
PCT-US93-09167-4

Query Match      100.0%; Score 3237; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLARALLICAVLALSHSTANPCSHPCONRGVCMVSGFDYKDCDCTRTGFGNGCSTPEEL 60
DB 1 MLARALLICAVLALSHSTANPCSHPCONRGVCMVSGFDYKDCDCTRTGFGNGCSTPEEL 60
QY 61 TRIKFLKPTNTVHYILTHFKGFNNVNNIPFLRNAINMSYVLTSRSHLIDSPPTYNADY 120
DB 61 TRIKFLKPTNTVHYILTHFKGFNNVNNIPFLRNAINMSYVLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAEFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
DB 121 GYKSWAEFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 180
QY 181 NMMAFAFQHTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFLKGGKMY 240
DB 181 NMMAFAFQHTHOFKTDHKGPAFTNGLGHGVDLNHIYGETLAROKRLRFLKGGKMY 240
QY 241 QIIDGEMTPPYVKTQDAEMITPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 300
DB 241 QIIDGEMTPPYVKTQDAEMITPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPPQS 300

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QY 301 VKQHEHWEGBDQFQTSRLIIIGETIKIVIEDYVOHLSGYHFKLKEPDELLFNKQFOYQ 360  
DB 301 VKQHEHWEGBDQFQTSRLIIIGETIKIVIEDYVOHLSGYHFKLKEPDELLFNKQFOYQ 360  
QY 361 NRIAAEFNTLYHWHPLPDTFQIHDOXNYQOFTYNNLSILHEGITOFEVSEFTROJAGRY 420  
DB 361 NRIAAEFNTLYHWHPLPDTFQIHDOXNYQOFTYNNLSILHEGITOFEVSEFTROJAGRY 420  
QY 421 AGGRNVPVAVOKVQASIDQSRQMKYOSFNEVYKRMFLKPYESFEELTGKEMSALEAL 480  
DB 421 AGGRNVPVAVOKVQASIDQSRQMKYOSFNEVYKRMFLKPYESFEELTGKEMSALEAL 480  
QY 481 YGDIADVELYPALVYKRPDAIFGETMVEVGAPEFLKGLMGVICSAPYWKSTFGGEV 540  
DB 481 YGDIADVELYPALVYKRPDAIFGETMVEVGAPEFLKGLMGVICSAPYWKSTFGGEV 540  
QY 541 GFOIINTASTOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDINFTVLKER 600  
DB 541 GFOIINTASTOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDINFTVLKER 600  
QY 601 STEL 604  
DB 601 STEL 604

## RESULT 8

US-08-487-753-5  
; Sequence 5, Application US/08487753  
; Patent No. 5807733  
; GENERAL INFORMATION:  
; APPLICANT: Young, Donald A.  
; APPLICANT: O'Banion, Michael K.  
; APPLICANT: Winn, Virginia D.  
; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2  
; TITLE OF INVENTION: FUSION PROTEINS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,753  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3996-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 604 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-487-753-5

Query Match 99.8%; Score 3230; DB 1; Length 604;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLARALLICAVLALSHNTANPCCSHPCONRGVCMVGFPDYKCDCTRTGFGYGENCSTPEFL 60  
DB 1 MLARALLICAVLALSHNTANPCCSHPCONRGVCMVGFPDYKCDCTRTGFGYGENCSTPEFL 60  
QY 61 TRIKFLKPTENTVHYILTHFKGFNNVYNNIPFLNNAIMSYL7TSRSHLIDSPPTYNADY 120  
DB 61 TRIKFLKPTENTVHYILTHFKGFNNVYNNIPFLNNAIMSYL7TSRSHLIDSPPTYNADY 120  
QY 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVYGGKQOLPDSNIEVKKLLRRRFPDPQGS 180  
DB 121 GYKSWAEFNSLSYTRALPVPDDCPTPLGVYGGKQOLPDSNIEVKKLLRRRFPDPQGS 180  
QY 181 NMFAFFAOFHTHOEFKTDHKKRGAFTNGIGHVDLNIYGETLARQRKLRFCKGRMY 240  
DB 181 NMFAFFAOFHTHOEFKTDHKKRGAFTNGIGHVDLNIYGETLARQRKLRFCKGRMY 240  
QY 241 QIIDGEMPTPVYKDQAEIITPPQVPEHLRFVAGQEVFGLVPGIMMYATIMREHNRVCD 300  
DB 241 QIIDGEMPTPVYKDQAEIITPPQVPEHLRFVAGQEVFGLVPGIMMYATIMREHNRVCD 300  
QY 301 VKQHEHWEGBDQFQTSRLIIIGETIKIVIEDYVOHLSGYHFKLKEPDELLFNKQFOYQ 360  
DB 301 VKQHEHWEGBDQFQTSRLIIIGETIKIVIEDYVOHLSGYHFKLKEPDELLFNKQFOYQ 360  
QY 361 NRIAAEFNTLYHWHPLPDTFQIHDOXNYQOFTYNNLSILHEGITOFEVSEFTROJAGRY 420  
DB 361 NRIAAEFNTLYHWHPLPDTFQIHDOXNYQOFTYNNLSILHEGITOFEVSEFTROJAGRY 420  
QY 421 AGGRNVPVAVOKVQASIDQSRQMKYOSFNEVYKRMFLKPYESFEELTGKEMSALEAL 480  
DB 421 AGGRNVPVAVOKVQASIDQSRQMKYOSFNEVYKRMFLKPYESFEELTGKEMSALEAL 480  
QY 481 YGDIADVELYPALVYKRPDAIFGETMVEVGAPEFLKGLMGVICSAPYWKSTFGGEV 540  
DB 481 YGDIADVELYPALVYKRPDAIFGETMVEVGAPEFLKGLMGVICSAPYWKSTFGGEV 540  
QY 541 GFOIINTASTOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDINFTVLKER 600  
DB 541 GFOIINTASTOSLICNNVKGCPFTSFVDPDELIKVTITNASSRSGLDINFTVLKER 600  
QY 601 STEL 604  
DB 601 STEL 604

## RESULT 9

US-08-480-065-5  
; Sequence 5, Application US/08480065  
; Patent No. 5837479  
; GENERAL INFORMATION:  
; APPLICANT: Young, Donald A.  
; APPLICANT: O'Banion, Michael K.  
; APPLICANT: Winn, Virginia D.  
; TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF  
; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,065  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

RESULT 10  
US-08-487-744-5  
? Sequence 5, Application US/08487744  
? Patent No. 6048850  
? GENERAL INFORMATION:  
? APPLICANT: Young, Donald A.  
? APPLICANT: O'Banion, Michael K.  
? APPLICANT: Wimm, Virginia D.

QY	1	MAARLLLCAYALALSTTANPCSSHPCQNRGVCMVSGVPDOYKCDCTRGFYGENCSTPEFL	60
Db	1	MAARLLLCAYALALSTTANPCSSHPCQNRGVCMVSGVPDOYKCDCTRGFYGENCSTPEFL	60
QY	61	TRIKFLKRPNTVHYILTHFKGFMVNVANNIFELRAIAMSUYLTSSHLIDSPPTNADY	120
Db	61	TRIKFLKRPNTVHYILTHFKGFMVNVANNIFELRAIAMSUYLTSSHLIDSPPTNADY	120
QY	121	GYSWEAKSNLSYTRRALPRVPDDCPTPLGVYGGKOLPDSNEIVEKLLRRKEIPDPQS	180
Db	121	GYSWEAKSNLSYTRRALPRVPDDCPTPLGVYGGKOLPDSNEIVEKLLRRKEIPDPQS	180
QY	181	NMFAFPAQHFTCCFKTDHKGPAFTNGLGHGVLDLNIYGETLAROKRLRLPKDGMKY	240
Db	181	NMFAFPAQHFTCCFKTDHKGPAFTNGLGHGVLDLNIYGETLAROKRLRLPKDGMKY	240
QY	241	QIIOGEMPRPYVKTOAMNIYRPVDEHLRFVAVGSEFVLGVLQMMYATITWLEHNRVCD	300
Db	241	QIIOGEMPRPYVKTOAMNIYRPVDEHLRFVAVGSEFVLGVLQMMYATITWLEHNRVCD	300
QY	301	VLKQHEPWEDEQFQTSRLILIGFTIKLIVEDYQHLGSGYFKLKEPDELLPNKQFOYO	360
Db	301	VLKQHEPWEDEQFQTSRLILIGFTIKLIVEDYQHLGSGYFKLKEPDELLPNKQFOYO	360
QY	361	NRIAAEPFLYTHMHPILPDTFQIHDOKNYOOOFIYNSILLEHGITQFVSEFTROIAGHY	420
Db	361	NRIAAEPFLYTHMHPILPDTFQIHDOKNYOOOFIYNSILLEHGITQFVSEFTROIAGHY	420
QY	421	AGGNVBPAYQKVSQASIDQSRQMKYQSFNEYRKRFMLKPYVSEFELGEXKMSALEYL	480
Db	421	AGGNVBPAYQKVSQASIDQSRQMKYQSFNEYRKRFMLKPYVSEFELGEXKMSALEYL	480
QY	481	YGDIDAVELYPALLVEKRPDPAIFGETMVEVGAEPDLKGLMGNYICSDPAYMKPSTFGGEV	540

Db 481 YGDDIDAVELYPALIVEKRPDAIFGETWVEGAPSLKGLMGNVICSPPAYWKSTFGGEV 540  
 QY 541 GFOIINTASISLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600  
 Db 541 GFOIINTASISLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

## RESULT 11

PCT-US93-09167-5  
 ; Sequence 5, Application PC/TUS9309167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Donald A.  
 ; APPLICANT: O'Banion, M. Kerry  
 ; APPLICANT: Winn, Virginia D.  
 ; TITLE OF INVENTION: Stably-Transformed Mammalian Cells  
 ; TITLE OF INVENTION: Expressing a Regulated, Inflammatory Cyclooxygenase  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merchant & Gould  
 ; STREET: 3100 Northwest Center  
 ; CITY: Minneapolis  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/09167  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Moessner, Warren D.  
 ; REGISTRATION NUMBER: 30,440  
 ; REFERENCE/DOCKET NUMBER: 8840.20-US-01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 612-332-5300  
 ; TELEFAX: 612-332-9081  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 604 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Amino acid sequence Human PGHS-2  
 ; PCT-US93-09167-5

Query Match 99.8%; Score 3230; DB 5; Length 604;

Best Local Similarity 99.8%; Pred. No. 0; Indels 0; Gaps 0;

Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MLARALLCAVALISHTANPCSCSHPCONRGVCMGVGDFQYKDCDCTRTGFGYENGSTPEFL 60  
 QY 1 MLARALLCAVALISHTANPCSCSHPCONRGVCMGVGDFQYKDCDCTRTGFGYENGSTPEFL 60  
 Db 1 MLARALLCAVALISHTANPCSCSHPCONRGVCMGVGDFQYKDCDCTRTGFGYENGSTPEFL 60  
 QY 61 TRIKLFKPTNTVHYILTHFKGFVNANNIPFLRNAMSYVLTSRSHLIDSPPTVANDY 120  
 Db 61 TRIKLFKPTNTVHYILTHFKGFVNANNIPFLRNAMSYVLTSRSHLIDSPPTVANDY 120  
 QY 121 GYKSWFAFSNLSYSTRALPVPVDDCPTPLGVGKKQLPDSNEIYEKLLRRKFTPDPOGS 180  
 Db 121 GYKSWFAFSNLSYSTRALPVPVDDCPTPLGVGKKQLPDSNEIYEKLLRRKFTPDPOGS 180  
 QY 121 GYKSWFAFSNLSYSTRALPVPVDDCPTPLGVGKKQLPDSNEIYEKLLRRKFTPDPOGS 180  
 Db 121 GYKSWFAFSNLSYSTRALPVPVDDCPTPLGVGKKQLPDSNEIYEKLLRRKFTPDPOGS 180  
 QY 181 NMFAFAQHTFHQFFKTDHKGPAFTNGLGHVLDNHIYGETTLARQKRLRFKDGKKMY 240  
 Db 181 NMFAFAQHTFHQFFKTDHKGPAFTNGLGHVLDNHIYGETTLARQKRLRFKDGKKMY 240

Db 181 NMFAFAQHTFHQFFKTDHKGPAFTNGLGHVLDNHIYGETTLARQKRLRFKDGKKMY 240  
 QY 241 QIIDGEMVPTVKTOEMITPVPOPEHLRPAVGQEVGLVGLMMYATIMLREHNRVCD 300  
 Db 241 QIIDGEMVPTVKTOEMITPVPOPEHLRPAVGQEVGLVGLMMYATIMLREHNRVCD 300  
 QY 301 VLKQHPPEWDEQLFOTSRLLIGETIKIVIEDVYQHLSGYFKLKPDELLFNKQFOYO 360  
 Db 301 VLKQHPPEWDEQLFOTSRLLIGETIKIVIEDVYQHLSGYFKLKPDELLFNKQFOYO 360  
 QY 361 NRIAAEFNTLYHMLPDPDQIHDQKNYQOFTYNNLSLLEHGLTQVESFTROIARV 420  
 Db 361 NRIAAEFNTLYHMLPDPDQIHDQKNYQOFTYNNLSLLEHGLTQVESFTROIARV 420  
 QY 421 AGGRVVPVAVQKVSQASIDOSROMKYQGFNEFRKRFMLKPYESFELTGKEMSALEAL 480  
 Db 421 AGGRVVPVAVQKVSQASIDOSROMKYQGFNEFRKRFMLKPYESFELTGKEMSALEAL 480  
 QY 481 YGDDIDAVELYPALIVEKRPDAIFGETWVEGAPSLKGLMGNVICSPPAYWKSTFGGEV 540  
 Db 481 YGDDIDAVELYPALIVEKRPDAIFGETWVEGAPSLKGLMGNVICSPPAYWKSTFGGEV 540  
 QY 541 GFOIINTASISLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600  
 Db 541 GFOIINTASISLICNNVKGCFSTFSVPDELLIKTVITINASSRSGDDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

## RESULT 12

US-09-919-060-5  
 ; Sequence 5, Application US/09919060  
 ; Patent No. 6638744  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wisniewski, Nancy  
 ; APPLICANT: Brandt, Kevin S.  
 ; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES  
 ; FILE REFERENCE: AD-1  
 ; CURRENT APPLICATION NUMBER: US/09/919,060  
 ; CURRENT FILING DATE: 2001-07-31  
 ; PRIOR APPLICATION NUMBER: 60/224,486  
 ; PRIOR FILING DATE: 2000-08-11  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 604  
 ; TYPE: PRT  
 ; ORGANISM: Canis familiaris  
 ; US-09-919-060-5

Query Match 91.7%; Score 2967; DB 4; Length 604;

Best Local Similarity 90.1%; Pred. No. 5; 6e-298;

Matches 544; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

Db 1 MLARALLCAVALISHTANPCSCSHPCONRGVCMGVGDFQYKDCDCTRTGFGYENGSTPEFL 60  
 QY 1 MLARALLCAVALISHTANPCSCSHPCONRGVCMGVGDFQYKDCDCTRTGFGYENGSTPEFL 60  
 Db 1 MLARALLCAVALISHTANPCSCSHPCONRGVCMGVGDFQYKDCDCTRTGFGYENGSTPEFL 60  
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 Db 61 TRIKLFKPTNTVHYILTHFKGFVNANNIPFLRNAMSYVLTSRSHLIDSPPTVANDY 120  
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 Db 121 GYKSWFAFSNLSYSTRALPVPVDDCPTPLGVGKKQLPDSNEIYEKLLRRKFTPDPOGS 180  
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 Db 121 GYKSWFAFSNLSYSTRALPVPVDDCPTPLGVGKKQLPDSNEIYEKLLRRKFTPDPOGS 180  
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 Db 181 NMFAFAQHTFHQFFKTDHKGPAFTNGLGHVLDNHIYGETTLARQKRLRFKDGKKMY 240



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 QY 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKEPDELLFNKQFOYQ 360  
 Db 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKEPDELLFNKQFOYQ 360  
 QY 361 NRIAEENLYHMHPLPDTFQIHDOCKNYQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
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 Db 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPFLKPYSPFEELTGKEMSALEAL 480  
 QY 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540  
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 Db 541 GFOIINTASIOSLIGNNVGCPFTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600  
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## RESULT 13

US-08-487-753-2  
 ; Sequence 2, Application US/08487753  
 ; Patent No. 5807733

## GENERAL INFORMATION:

APPLICANT: Young, Donald A.  
 APPLICANT: O'Banion, Michael K.  
 TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2  
 TITLE OF INVENTION: FUSION PROTEINS  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,753  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3996-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELETYPE: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-487-753-2

Query Match

88.8%; Score 2873; DB 1; Length 604;

Best Local Similarity 86.8%; Pred. No. 3e-288;  
 Matches 524; Conservative 39; Mismatches 41; Indels 0; Gaps 0;  
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 Db 1 MLRAVILCALGILSQAANPCSNPCQNRGECSTGPDQYKCDCTRTGFGNCSTPEFL 60  
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 Db 61 TRIKLLKPPNTVHYILTHFKGFNVVNNIPILRNALMSYVLTSSRLIDSPPTVADY 120  
 QY 121 GYSWAEFSLSYTTALPVPDDCPTPIGVKKKQOLPDSNEVEYKLLFRKTIPTDQGS 180  
 Db 121 GYSWAEFSLSYTTALPVPDDCPTPIGVKKKQOLPDSNEVEYKLLFRKTIPTDQGS 180  
 QY 181 NMWFAFQHTHOFKTDHKGPAFTNGILGSHVDLNIHYGETLARQKRLFKDGKLY 240  
 Db 181 NMWFAFQHTHOFKTDHKGPAFTNGILGSHVDLNIHYGETLARQKRLFKDGKLY 240  
 QY 241 QIIDGEMYPPTVKDQOAEMLYPPQVEHLRFVAGQEVGIVPGIMYATITWLRHNRYCD 300  
 Db 241 QVIDGEVYPTVKDQOAEMLYPPQVEHLRFVAGQEVGIVPGIMYATITWLRHNRYCD 300  
 QY 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKEPDELLFNKQFOYQ 360  
 Db 301 VLKQEHPEWDEQOLFQTSRLILIGETIKIVIEDYVQHLGSGYHFKLKEPDELLFNKQFOYQ 360  
 QY 361 NRIAEENLYHMHPLPDTFQIHDOCKNYQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
 Db 361 NRIAEENLYHMHPLPDTFQIHDOCKNYQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
 QY 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPFLKPYSPFEELTGKEMSALEAL 480  
 Db 421 AGGRNVPAAVQAKASIDQSRQMKYOSFNEVYKRPFLKPYSPFEELTGKEMSALEAL 480  
 QY 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540  
 Db 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPFSLKGLMGNVCSPAYMKSTFGGEV 540  
 QY 541 GFOIINTASIOSLIGNNVGCPFTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600  
 Db 541 GFOIINTASIOSLIGNNVGCPFTSFVSVPDELLIKVTINASSRSGLDINPTVLLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

## RESULT 14

US-08-480-065-2  
 ; Sequence 2, Application US/08480065  
 ; Patent No. 5837479

## GENERAL INFORMATION:

APPLICANT: Young, Donald A.  
 APPLICANT: O'Banion, Michael K.  
 TITLE OF INVENTION: SCREENING ASSAYS FOR INHIBITORS OF  
 TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,065

FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3996-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELETYPE: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-480-065-2

Query Match 88.8%; Score 2873; DB 2; Length 604;  
 Best Local Similarity 86.8%; Pred. No. 3e-288; Mismatches 41; Indels 0; Gaps 0;  
 Matches 524; Conservative 39;

1 M L A R A L L C A V A L A S H T A N P C C S H P C O N R G V C M S V G F D O Y K D C T R T G Y G E N C S T P E F L 60  
 1 M L F R A V L L C A L G L S Q A A N P C C S N P C O N R G E C M S T G F D O Y K D C T R T G Y G E N C T T P E F L 60  
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 121 G Y K S W E A F S N L S Y T T R A L P R V A D C P T P G V K G K N K E L P D S K E V L E K V L R R E F I P D P Q S 180  
 181 N M M F A F A Q H T H O F P T D H K R G P A F T N G L G H G V D L N H I Y G E T L A R Q R K L R F D G R K Y 240  
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 241 Q I I D G E M Y P P T V K D T O A E M I Y P P Q V P E H L R F A V G E V F G I V P G I M A T A T I W L E H N R V C D 300  
 241 Q V I G G E Y P P T V K D T O V E M I Y P P H I P E N L Q F A V G E V F G I V P G I M A T A T I W L E H N R V C D 300  
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 301 I L K O E H E M G D E O L F O T S R L I L G E T I K I V I E D V V O H L S G H F L K A K D P E L L F N K O F O Y Q 360  
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 QY 601 S T E L 604  
 DB 601 S T E L 604

O

RESULT 15  
 US-08-487-744-2  
 Sequence 2, Application US/08487744  
 Patent No. 6048850  
 GENERAL INFORMATION:  
 APPLICANT: Young, Donald A.

APPLICANT: O'Banion, Michael K.  
 APPLICANT: Winn, Virginia D.  
 TITLE OF INVENTION: METHODS FOR INHIBITING PROSTAGLANDIN  
 TITLE OF INVENTION: SYNTHESIS IN A MAMMALIAN HOST  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,744

FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3996-013  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELETYPE: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-487-744-2

Query Match 88.8%; Score 2873; DB 3; Length 604;  
 Best Local Similarity 86.8%; Pred. No. 3e-288; Mismatches 41; Indels 0; Gaps 0;  
 Matches 524; Conservative 39;

1 M L A R A L L C A V A L A S H T A N P C C S H P C O N R G V C M S V G F D O Y K D C T R T G Y G E N C S T P E F L 60  
 1 M L F R A V L L C A L G L S Q A A N P C C S N P C O N R G E C M S T G F D O Y K D C T R T G Y G E N C T T P E F L 60  
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 301 I L K O E H E M G D E O L F O T S R L I L G E T I K I V I E D V V O H L S G H F L K A K D P E L L F N K O F O Y Q 360  
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 361 N R I A S E N T L Y H M P L P D T F N I E D Q E Y S F K O F L Y N N S I L L E H G L T O F V E S F T R O I A G R V 420  
 421 A G G R N V P A V Q K Y S O A S I D S R O M K Y O S F N E Y R K R F E M L K P E S F E E L T G E K E M A E L A L 480  
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Sun Apr 25 18:03:17 2004

us-08-064-271-10.ra1

Page 11

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Db 541 GFKIINTASIOSLGNWVGCPFTSRVDPDPPTKATINASASHRLDINPTVLKRR 600
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Db 601 STEL 604
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8/10/21

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2004, 07:21:12 ; Search time 73 Seconds

(without alignments)  
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Title: US-08-064-271-10

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Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*

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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	3237	100.0	604	12	US-10-211-462-133
4	3237	100.0	604	12	US-10-170-385-237
5	3237	100.0	604	14	US-10-027-961A-18
6	3237	100.0	604	14	US-10-021-660-109
7	3237	100.0	604	15	US-10-260-937-22
8	3237	100.0	604	15	US-10-295-027-32
9	3237	100.0	604	15	US-10-373-801-30
10	2971	91.8	604	15	US-10-260-937-27
11	2967	91.7	604	9	US-09-919-060-5
12	2958	90.8	604	10	US-09-949-293-30
13	2938	90.8	604	15	US-10-260-937-26
14	2923	90.3	604	15	US-10-260-937-25
15	2902	89.7	599	10	US-09-949-293-31

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17	2892	89.3	604	15	US-10-260-937-28	Sequence 26, Appl
18	2881.5	89.0	603	10	US-09-949-293-32	Sequence 32, Appl
19	2881.5	89.0	603	15	US-10-260-937-23	Sequence 23, Appl
20	2881.5	89.0	603	15	US-10-260-937-24	Sequence 24, Appl
21	2877	88.9	604	10	US-09-949-293-26	Sequence 26, Appl
22	2873	88.8	604	15	US-10-260-937-29	Sequence 29, Appl
23	2868	88.6	604	15	US-09-953-067A-8	Sequence 8, Appl
24	2868	88.6	604	15	US-10-260-937-30	Sequence 30, Appl
25	2828	87.4	604	15	US-10-260-937-46	Sequence 46, Appl
26	2741	84.7	582	15	US-10-260-937-35	Sequence 35, Appl
27	2726.5	84.2	603	15	US-10-260-937-31	Sequence 31, Appl
28	2629	81.2	544	10	US-09-949-293-29	Sequence 29, Appl
29	2525	78.0	544	10	US-09-949-293-27	Sequence 27, Appl
30	2425	74.9	607	15	US-10-260-937-33	Sequence 33, Appl
31	2417	74.7	607	15	US-10-260-937-32	Sequence 32, Appl
32	2045.5	63.2	599	10	US-09-953-067A-3	Sequence 3, Appl
33	2037	62.9	599	12	US-10-382-248-6	Sequence 6, Appl
34	2037	62.9	599	14	US-10-097-340-264	Sequence 264, App
35	2037	62.9	599	15	US-10-260-937-47	Sequence 47, Appl
36	2037	62.9	599	15	US-10-260-937-52	Sequence 52, Appl
37	2036.5	62.9	602	15	US-10-260-937-15	Sequence 15, Appl
38	2035.5	62.9	629	15	US-10-260-937-60	Sequence 60, Appl
39	2029.5	62.7	633	9	US-09-919-060-13	Sequence 13, Appl
40	2029.5	62.7	633	15	US-10-260-937-7	Sequence 7, Appl
41	2029.5	62.7	633	15	US-09-953-067A-7	Sequence 7, Appl
42	2027.5	62.6	602	15	US-10-260-937-51	Sequence 51, Appl
43	2027.5	62.6	603	15	US-10-260-937-58	Sequence 58, Appl
44	2026.5	62.6	603	15	US-10-260-937-54	Sequence 54, Appl
45	2024.5	62.5	598	15	US-10-260-937-54	Sequence 54, Appl

## ALIGNMENTS

RESULT 1  
US-09-953-067A-4  
; Sequence 4, Application US/09953067A  
; Publication No. US20030082141A1  
; GENERAL INFORMATION:  
; APPLICANT: O'CONNOR, J. Patrick  
; TITLE OF INVENTION: COX-2 FUNCTION AND WOUND HEALING  
; FILE REFERENCE: 267/043  
; CURRENT APPLICATION NUMBER: US/09/953,067A  
; CURRENT FILING DATE: 2001-09-11  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-953-067A-4

Query Match 100.0%; Score 3237; DB 10; Length 604;  
Best Local Similarity 100.0%; Pred. No. 6.1e-313;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MARALLCAVALSHSTANPCCHPQNRGVCMVSGVDQYKDCDCTRTGFGNCSTPEFL 60
DB	1	MARALLCAVALSHSTANPCCHPQNRGVCMVSGVDQYKDCDCTRTGFGNCSTPEFL 60
QY	61	TRIKLPLKPTNTVHYILTHFGFMVWVNNIPILRAIMSVYLTSSHLIDSPPTNADY 120
DB	61	TRIKLPLKPTNTVHYILTHFGFMVWVNNIPILRAIMSVYLTSSHLIDSPPTNADY 120
QY	121	GYSKMEAFSNLSYTRALPVPDDCPTPLGVKSKOLPDSNEIVKLLLRKFIIPPOGS 180
DB	121	GYSKMEAFSNLSYTRALPVPDDCPTPLGVKSKOLPDSNEIVKLLLRKFIIPPOGS 180
QY	181	NNMFAFAQHFPHTQFKTKHKGPAFTNGLGHGVNDLNHYGTGLAQRTKLRLKDGKMKY 240
DB	181	NNMFAFAQHFPHTQFKTKHKGPAFTNGLGHGVNDLNHYGTGLAQRTKLRLKDGKMKY 240

```
Qy 241 QIIDGEMYPPTVKDQTOAEMITPPOVPEHLRFPAVGQEVFGLVPGIMMYATTIWLREHNVCD 300
Db 241 QIIDGEMYPPTVKDQTOAEMITPPOVPEHLRFPAVGQEVFGLVPGIMMYATTIWLREHNVCD 300
Qy 301 VLKQEHHEWGDQOLFQTSRLLILIGETIKIYIEDVVOHLSGYHFKLKFDPPELLFNKQFOYQ 360
Db 301 VLKQEHHEWGDQOLFQTSRLLILIGETIKIYIEDVVOHLSGYHFKLKFDPPELLFNKQFOYQ 360
Qy 361 NR1AAEFNTLYHMHPLLPDFTQIHDOKNYQOFTYNNSSILLEHGITQFVESFTQIAGRV 420
Db 361 NR1AAEFNTLYHMHPLLPDFTQIHDOKNYQOFTYNNSSILLEHGITQFVESFTQIAGRV 420
Qy 421 AGGNVPPAVQKVSQASIDSRQMKYOSFNEYRRKFMFKPYESEPEELLTGEKEMSALEAL 480
Db 421 AGGNVPPAVQKVSQASIDSRQMKYOSFNEYRRKFMFKPYESEPEELLTGEKEMSALEAL 480
Qy 481 YGDDDAVELYPALLVEKRPDAIFGETMVEYGAFPSLKLGMGNVICSPAYWKPSFTPGGEV 540
Db 481 YGDDDAVELYPALLVEKRPDAIFGETMVEYGAFPSLKLGMGNVICSPAYWKPSFTPGGEV 540
Qy 541 GFOIINTASIOSLICNNVKGCEFTSFVDPDELIKVTITINASSRSGLDINPTVLLKER 600
Db 541 GFOIINTASIOSLICNNVKGCEFTSFVDPDELIKVTITINASSRSGLDINPTVLLKER 600
Qy 601 STEL 604
Db 601 STEL 604
```

```
RESULT 2
US-09-949-293-33
; Sequence 33, Application US/09949293
; Publication No. US20030082550A1
; GENERAL INFORMATION:
; APPLICANT: Thomann, Hans-Ulrich
; APPLICANT: Wall, Kristian
; APPLICANT: Fitzgerald, Michael
; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE
; FILE REFERENCE: TECH01-07
; CURRENT APPLICATION NUMBER: US/09/949,293
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/231,250
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-293-33
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Query Match 100.0%; Score 3237; DB 10; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 M1ARALLICAVIALSHTANPCCSHPCQNRGVCMVGFDQYKDCDCTRTGFGNGCSTPEL 60
Db 1 M1ARALLICAVIALSHTANPCCSHPCQNRGVCMVGFDQYKDCDCTRTGFGNGCSTPEL 60
Qy 61 TRIKFLKPTPTVYIILTFKGFNNVNNIPEFLNNAISYVLTSRSHLIDSPPTYNADY 120
Db 61 TRIKFLKPTPTVYIILTFKGFNNVNNIPEFLNNAISYVLTSRSHLIDSPPTYNADY 120
Qy 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKQKQLPDSNEIVEKLLRRKFIPDPQGS 180
Db 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKQKQLPDSNEIVEKLLRRKFIPDPQGS 180
Qy 181 NMWAFPAQHTHOFKPDHKGPAFTNGLGHVGLNHIYGETLAROKRLRFKQGXMKY 240
Db 181 NMWAFPAQHTHOFKPDHKGPAFTNGLGHVGLNHIYGETLAROKRLRFKQGXMKY 240
Qy 241 QIIDGEMYPPTVKDQTOAEMITPPOVPEHLRFPAVGQEVFGLVPGIMMYATTIWLREHNVCD 300
Db 241 QIIDGEMYPPTVKDQTOAEMITPPOVPEHLRFPAVGQEVFGLVPGIMMYATTIWLREHNVCD 300
```

```
Db 241 QIIDGEMYPPTVKDQTOAEMITPPOVPEHLRFPAVGQEVFGLVPGIMMYATTIWLREHNVCD 300
Qy 301 VLKQEHHEWGDQOLFQTSRLLILIGETIKIYIEDVVOHLSGYHFKLKFDPPELLFNKQFOYQ 360
Db 301 VLKQEHHEWGDQOLFQTSRLLILIGETIKIYIEDVVOHLSGYHFKLKFDPPELLFNKQFOYQ 360
Qy 361 NR1AAEFNTLYHMHPLLPDFTQIHDOKNYQOFTYNNSSILLEHGITQFVESFTQIAGRV 420
Db 361 NR1AAEFNTLYHMHPLLPDFTQIHDOKNYQOFTYNNSSILLEHGITQFVESFTQIAGRV 420
Qy 421 AGGNVPPAVQKVSQASIDSRQMKYOSFNEYRRKFMFKPYESEPEELLTGEKEMSALEAL 480
Db 421 AGGNVPPAVQKVSQASIDSRQMKYOSFNEYRRKFMFKPYESEPEELLTGEKEMSALEAL 480
Qy 481 YGDDDAVELYPALLVEKRPDAIFGETMVEYGAFPSLKLGMGNVICSPAYWKPSFTPGGEV 540
Db 481 YGDDDAVELYPALLVEKRPDAIFGETMVEYGAFPSLKLGMGNVICSPAYWKPSFTPGGEV 540
Qy 541 GFOIINTASIOSLICNNVKGCEFTSFVDPDELIKVTITINASSRSGLDINPTVLLKER 600
Db 541 GFOIINTASIOSLICNNVKGCEFTSFVDPDELIKVTITINASSRSGLDINPTVLLKER 600
Qy 601 STEL 604
Db 601 STEL 604
```

```
RESULT 3
US-10-211-462-133
; Sequence 133, Application US/10211462
; Publication No. US2004003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-133
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```
Query Match 100.0%; Score 3237; DB 12; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 M1ARALLICAVIALSHTANPCCSHPCQNRGVCMVGFDQYKDCDCTRTGFGNGCSTPEL 60
Db 1 M1ARALLICAVIALSHTANPCCSHPCQNRGVCMVGFDQYKDCDCTRTGFGNGCSTPEL 60
Qy 61 TRIKFLKPTPTVYIILTFKGFNNVNNIPEFLNNAISYVLTSRSHLIDSPPTYNADY 120
Db 61 TRIKFLKPTPTVYIILTFKGFNNVNNIPEFLNNAISYVLTSRSHLIDSPPTYNADY 120
Qy 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKQKQLPDSNEIVEKLLRRKFIPDPQGS 180
Db 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVGKQKQLPDSNEIVEKLLRRKFIPDPQGS 180
```

```

QY 181 NMFAFFAQTHTQFQKTDHKGPAFTNGLGHVLDLNIYGETTLARQRLRLFQDGMKY 240
DB 181 NMFAFFAQTHTQFQKTDHKGPAFTNGLGHVLDLNIYGETTLARQRLRLFQDGMKY 240
QY 241 QIIDGEMPTVKDQAEIMIPPOVEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
DB 241 QIIDGEMPTVKDQAEIMIPPOVEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
QY 301 VLKQHPHMGDEQLFQTSRLILIGETIKIVIEDYQHLSGYHFKLKFDELLFNQFOFOY 360
DB 301 VLKQHPHMGDEQLFQTSRLILIGETIKIVIEDYQHLSGYHFKLKFDELLFNQFOFOY 360
QY 361 NR1AAEFNTLYMHMLPDTFOIHDQKYNQOQFIYNNLSILBHGITQFVESFTROIAGRV 420
DB 361 NR1AAEFNTLYMHMLPDTFOIHDQKYNQOQFIYNNLSILBHGITQFVESFTROIAGRV 420
QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYOSFNEYRKRPMKPYESFEELTGEKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYOSFNEYRKRPMKPYESFEELTGEKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGMGNVICSAPYMKPSTFGGEV 540
DB 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGMGNVICSAPYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELLIKVTITNASSRSGLDINPTVLLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELLIKVTITNASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

## RESULT 4

```

US-10-170-385-237
; Sequence 237, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-237

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```

Query Match 100.0%; Score 3237; DB 12; Length 604;
Best Local Similarity 100.0%; Pred. No. 6,1e-313;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLARALLCAVVALSHATNPGCSHPCONRGVCMVSGFDQKCDCTRTGFGNCSPTPEFL 60
DB 1 MLARALLCAVVALSHATNPGCSHPCONRGVCMVSGFDQKCDCTRTGFGNCSPTPEFL 60

```

```

QY 61 TRIKLEKPTNTVAHILTHFKGFNNVYNNIPELNAIMSVYLTSRSHLIDSPPTYNADY 120
DB 61 TRIKLEKPTNTVAHILTHFKGFNNVYNNIPELNAIMSVYLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAENSLSYTRALPVPDDCPTPLGVGKKQLPDSNIEVKLLRRFEIDPQOS 180
DB 121 GYKSWAENSLSYTRALPVPDDCPTPLGVGKKQLPDSNIEVKLLRRFEIDPQOS 180
QY 181 NMFAFFAQTHTQFQKTDHKGPAFTNGLGHVLDLNIYGETTLARQRLRLFQDGMKY 240
DB 181 NMFAFFAQTHTQFQKTDHKGPAFTNGLGHVLDLNIYGETTLARQRLRLFQDGMKY 240
QY 241 QIIDGEMPTVKDQAEIMIPPOVEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
DB 241 QIIDGEMPTVKDQAEIMIPPOVEHLRFVAVGVEGLVPGLMVYATIMLRHNRCVD 300
QY 301 VLKQHPHMGDEQLFQTSRLILIGETIKIVIEDYQHLSGYHFKLKFDELLFNQFOFOY 360
DB 301 VLKQHPHMGDEQLFQTSRLILIGETIKIVIEDYQHLSGYHFKLKFDELLFNQFOFOY 360
QY 361 NR1AAEFNTLYMHMLPDTFOIHDQKYNQOQFIYNNLSILBHGITQFVESFTROIAGRV 420
DB 361 NR1AAEFNTLYMHMLPDTFOIHDQKYNQOQFIYNNLSILBHGITQFVESFTROIAGRV 420
QY 421 AGGRNVPPAVQKVSQASIDQSRQMKYOSFNEYRKRPMKPYESFEELTGEKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDQSRQMKYOSFNEYRKRPMKPYESFEELTGEKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGMGNVICSAPYMKPSTFGGEV 540
DB 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEVGAFFSLKGMGNVICSAPYMKPSTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELLIKVTITNASSRSGLDINPTVLLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVDPDELLIKVTITNASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

## RESULT 5

```

US-10-027-961A-18
; Sequence 18, Application US/10027961A
; Publication No. US20030032789A1
; GENERAL INFORMATION:
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; FILE REFERENCE: 19029PCADA
; CURRENT APPLICATION NUMBER: US/10/027,961A
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/599,781
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 08/930,589
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: PCT/CA94/00501
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/084,033
; PRIOR FILING DATE: 1993-09-27
; PRIOR APPLICATION NUMBER: 08/064,271
; PRIOR FILING DATE: 1993-05-06
; PRIOR APPLICATION NUMBER: 07/994,760
; PRIOR FILING DATE: 1992-12-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Human
US-10-027-961A-18

```

Query Match 100.0%; Score 3237; DB 14; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-313;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MLARALLCAVLAISHANPCSSHPCCNRGVCMSVGFQYKCDCTRTGFGYENCSTPEFL 60
DB 1 MLARALLCAVLAISHANPCSSHPCCNRGVCMSVGFQYKCDCTRTGFGYENCSTPEFL 60
OY 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPLRLNAMSYYLTSRSHLIDSPPTVADY 120
DB 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPLRLNAMSYYLTSRSHLIDSPPTVADY 120
OY 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
OY 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
OY 181 NMFAFPAQHTHOFKTDHKGPAFTNGLGVDLNIYGETLARQKRLPFDGKKMY 240
DB 181 NMFAFPAQHTHOFKTDHKGPAFTNGLGVDLNIYGETLARQKRLPFDGKKMY 240
OY 241 QIIDGEMYPPTVKDQAMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
DB 241 QIIDGEMYPPTVKDQAMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
OY 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
OY 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYOQFIYNSILLEGITQEVESFTROIARV 420
DB 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYOQFIYNSILLEGITQEVESFTROIARV 420
OY 421 AGRNVPAPVQKVSQASIDSRQMKYQSFNRYKRPMLKPYHSFELTGEKMSLAL 480
DB 421 AGRNVPAPVQKVSQASIDSRQMKYQSFNRYKRPMLKPYHSFELTGEKMSLAL 480
OY 481 YGDDDAVELYPLLVEKRPDAIFGETWVEGAPSLKGMGNVCSPAYWKPSTFGGEV 540
DB 481 YGDDDAVELYPLLVEKRPDAIFGETWVEGAPSLKGMGNVCSPAYWKPSTFGGEV 540
OY 541 GFOINTASIOSLICNNVKGCFSTFSVDPDELLITVTINASSRSGDDIDNPVTLKER 600
DB 541 GFOINTASIOSLICNNVKGCFSTFSVDPDELLITVTINASSRSGDDIDNPVTLKER 600
OY 601 STEL 604
DB 601 STEL 604

```

RESULT 6  
 US-10-021-660-109  
 ; Sequence 109, Application US/10021660  
 ; Publication No. US20030152926A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Glynn, Susan R.  
 ; APPLICANT: EOS Biotechnology, Inc.  
 ; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,  
 ; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
 ; FILE REFERENCE: 018501-000710US  
 ; CURRENT APPLICATION NUMBER: US/10/021,660  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US/09/784,356  
 ; PRIOR FILING DATE: 2001-02-14  
 ; PRIOR APPLICATION NUMBER: US 09/637,977  
 ; NUMBER OF SEQ ID NOS: 135  
 ; SOFTWARE: FaSTSeq for Windows Version 3.0  
 ; SEQ ID NO 109  
 ; LENGTH: 604  
 ; TYPE: PRT

ORGANISM: Homo sapiens  
 US-10-021-660-109

Query Match 100.0%; Score 3237; DB 14; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-313;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MLARALLCAVLAISHANPCSSHPCCNRGVCMSVGFQYKCDCTRTGFGYENCSTPEFL 60
DB 1 MLARALLCAVLAISHANPCSSHPCCNRGVCMSVGFQYKCDCTRTGFGYENCSTPEFL 60
OY 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPLRLNAMSYYLTSRSHLIDSPPTVADY 120
DB 61 TRIKLFKPTNTVHYILLTHEKGFNNVNNIPLRLNAMSYYLTSRSHLIDSPPTVADY 120
OY 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
OY 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPVPVDDCPPLGKGGKQPLDSNEIYEKLLRRKFLPDPQGS 180
OY 181 NMFAFPAQHTHOFKTDHKGPAFTNGLGVDLNIYGETLARQKRLPFDGKKMY 240
DB 181 NMFAFPAQHTHOFKTDHKGPAFTNGLGVDLNIYGETLARQKRLPFDGKKMY 240
OY 241 QIIDGEMYPPTVKDQAMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
DB 241 QIIDGEMYPPTVKDQAMIVPQVBEHLRPAVGQEVGLVPGIMVATIMLRHNRYCD 300
OY 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWSGBOUFGTSRLILIGETIKIVIEDVYQHLSGVHFKLKPDELLFNKQFOYQ 360
OY 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYOQFIYNSILLEGITQEVESFTROIARV 420
DB 361 NRIAEFNTLYHMHPLPDTFQIHDQKXNYOQFIYNSILLEGITQEVESFTROIARV 420
OY 421 AGRNVPAPVQKVSQASIDSRQMKYQSFNRYKRPMLKPYHSFELTGEKMSLAL 480
DB 421 AGRNVPAPVQKVSQASIDSRQMKYQSFNRYKRPMLKPYHSFELTGEKMSLAL 480
OY 481 YGDDDAVELYPLLVEKRPDAIFGETWVEGAPSLKGMGNVCSPAYWKPSTFGGEV 540
DB 481 YGDDDAVELYPLLVEKRPDAIFGETWVEGAPSLKGMGNVCSPAYWKPSTFGGEV 540
OY 541 GFOINTASIOSLICNNVKGCFSTFSVDPDELLITVTINASSRSGDDIDNPVTLKER 600
DB 541 GFOINTASIOSLICNNVKGCFSTFSVDPDELLITVTINASSRSGDDIDNPVTLKER 600
OY 601 STEL 604
DB 601 STEL 604

```

RESULT 7  
 US-10-260-937-22  
 ; Sequence 22, Application US/10260937  
 ; Publication No. US20030220306A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Simmons, Daniel  
 ; APPLICANT: Chandrasekharan, N. Vishvanath  
 ; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
 ; TITLE OF INVENTION: METHODS OF USE  
 ; FILE REFERENCE: 07913-007001  
 ; CURRENT APPLICATION NUMBER: US/10/260,937  
 ; PRIOR FILING DATE: 2002-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/326,133  
 ; PRIOR FILING DATE: 2001-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/373,225  
 ; PRIOR FILING DATE: 2002-04-15  
 ; PRIOR APPLICATION NUMBER: US 60/373,661  
 ; PRIOR FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: US 60/411,575  
 ; NUMBER OF SEQ ID NOS: 89



SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 22  
 LENGTH: 604  
 TYPE: PR1  
 ORGANISM: Homo sapiens  
 US-10-260-937-22

Query Match 100.0%; Score 3237; DB 15; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 6,1e-313;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MABALLCAVALALSTANPCSSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
DB 1 MABALLCAVALALSTANPCSSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
QY 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAISYVLTSSHLIDSPPTYNADY 120
DB 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAISYVLTSSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
DB 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDEMYPPTVKDQOAMITPPQVEHRLPRAVGQEVFGLVGLMMYATIMLREHNRVCD 300
DB 241 QIIDEMYPPTVKDQOAMITPPQVEHRLPRAVGQEVFGLVGLMMYATIMLREHNRVCD 300
QY 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAEFNTLVHMHLPDPTFOIHQKKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
DB 361 NRIAEFNTLVHMHLPDPTFOIHQKKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYSPFELTGEKMSALEL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYSPFELTGEKMSALEL 480
QY 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPSLKGLMGNTVCSPAYMKSFTFGGEV 540
DB 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPSLKGLMGNTVCSPAYMKSFTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVSPDELIKTVITINASSRSGLDINPTVLKER 600
DB 541 GFOIINTASIOSLICNNVKGCPFTSFVSPDELIKTVITINASSRSGLDINPTVLKER 600
QY 601 STEL 604
DB 601 STEL 604

```

RESULT 8  
 US-10-295-027-32

Sequence 32, Application US/10295027  
 Publication No. US2003023250A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel  
 APPLICANT: Aziz, Natasha  
 APPLICANT: Ginsberg, Wendy M.  
 APPLICANT: Gish, Kurt C.  
 APPLICANT: Glynn, Richard  
 APPLICANT: Hevezi, Peter A.  
 APPLICANT: Mack, David H.  
 APPLICANT: Murray, Richard  
 APPLICANT: Watson, Susan R.  
 APPLICANT: Bos Biotechnology, Inc.  
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501-012500US  
 CURRENT APPLICATION NUMBER: US/10/295,027  
 PRIOR FILING DATE: 2002-11-13  
 PRIOR APPLICATION NUMBER: US 09/663,733  
 PRIOR FILING DATE: 2000-09-15  
 PRIOR APPLICATION NUMBER: US 60/350,666  
 PRIOR FILING DATE: 2001-11-13  
 PRIOR APPLICATION NUMBER: US 60/335,394  
 PRIOR FILING DATE: 2001-11-15  
 PRIOR APPLICATION NUMBER: US 60/332,464  
 PRIOR FILING DATE: 2001-11-21  
 PRIOR APPLICATION NUMBER: US 60/334,393  
 PRIOR FILING DATE: 2001-11-29  
 PRIOR APPLICATION NUMBER: US 60/340,376  
 PRIOR FILING DATE: 2001-12-14  
 PRIOR APPLICATION NUMBER: US 60/347,211  
 PRIOR FILING DATE: 2002-01-08  
 PRIOR APPLICATION NUMBER: US 60/347,349  
 PRIOR FILING DATE: 2002-01-10  
 PRIOR APPLICATION NUMBER: US 60/355,250  
 PRIOR FILING DATE: 2002-02-08  
 PRIOR APPLICATION NUMBER: US 60/356,714  
 PRIOR FILING DATE: 2002-02-13  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 1386  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 32  
 LENGTH: 604  
 TYPE: PR1  
 ORGANISM: Homo sapiens  
 US-10-295-027-32

Query Match 100.0%; Score 3237; DB 15; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 6,1e-313;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MABALLCAVALALSTANPCSSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
DB 1 MABALLCAVALALSTANPCSSHPCQNGVCMGVGFDDYKDCDCTRTGYGNCSTPEL 60
QY 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAISYVLTSSHLIDSPPTYNADY 120
DB 61 TRIKLEKPTVTYVYIITHEKGFNNVNNIPELRNAISYVLTSSHLIDSPPTYNADY 120
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
DB 121 GYKSWFAFNSLSYTRALPPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIDPQGS 180
QY 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
DB 181 NMMAFAFQHFTHQFETDHRKGPFTNGLGHVLDNIHYGETLARQRKRLFKDGKMKY 240
QY 241 QIIDEMYPPTVKDQOAMITPPQVEHRLPRAVGQEVFGLVGLMMYATIMLREHNRVCD 300
DB 241 QIIDEMYPPTVKDQOAMITPPQVEHRLPRAVGQEVFGLVGLMMYATIMLREHNRVCD 300
QY 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
DB 301 VLKQHPHWDQOLFQTSRLIIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFOYQ 360
QY 361 NRIAEFNTLVHMHLPDPTFOIHQKKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
DB 361 NRIAEFNTLVHMHLPDPTFOIHQKKNYQOFTYNNLSILHEGITTQVESTTRQIARV 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYSPFELTGEKMSALEL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYOSFNEYRKRFMLKPYSPFELTGEKMSALEL 480
QY 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPSLKGLMGNTVCSPAYMKSFTFGGEV 540
DB 481 YGIDDAVELYPALVEKRPDAIFGETWVEGAPSLKGLMGNTVCSPAYMKSFTFGGEV 540
QY 541 GFOIINTASIOSLICNNVKGCPFTSFVSPDELIKTVITINASSRSGLDINPTVLKER 600

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Db 541 GFOINTASTIQLICNNVKGCPFTSPVDPBELIKVTITINASSRSGLDINPTVLKGR 600

QY 601 STEL 604  
Db 601 STEL 604

## RESULT 9

US-10-373-801-30  
; Sequence 30, Application US/10373801  
; Publication No. US20040005644A1  
; GENERAL INFORMATION:  
; APPLICANT: Viba Pharmaceutical (USA)  
; TITLE OF INVENTION: Method and composition for detection and treatment of breast cancer  
; FILE REFERENCE: 12399.00  
; CURRENT APPLICATION NUMBER: US/10/373,801  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO: 30  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-373-801-30

Query Match 100.0%; Score 3237; DB 15; Length 604;  
Best Local Similarity 100.0%; Pred. No. 6.1e-313; Indels 0; Gaps 0;  
Matches 604; Conservative 0; Mismatches 0;

QY 1 MLARALLCAVALASTHAPCCSHPCQNGVCMVSGVDFQYKDCDCTRTGFGNGCSTPEEL 60  
Db 1 MLARALLCAVALASTHAPCCSHPCQNGVCMVSGVDFQYKDCDCTRTGFGNGCSTPEEL 60  
QY 61 TRIKLFLKPTPTVNHILTHFGKFMVNVNIPFLRAIMSIVLTSSHLIDSPPTYNADY 120  
Db 61 TRIKLFLKPTPTVNHILTHFGKFMVNVNIPFLRAIMSIVLTSSHLIDSPPTYNADY 120  
QY 121 GYKSWAFNSLYTRALPVPVDDCPTPLGVKGGKOLPDSNETVEKLLLRKFIIPDQGS 180  
Db 121 GYKSWAFNSLYTRALPVPVDDCPTPLGVKGGKOLPDSNETVEKLLLRKFIIPDQGS 180  
QY 181 NMMAFAFHQFTHQFRTDHRKGRPAFTNGIGHGVNDINHLYGETLAROKRLRFKDGKMY 240  
Db 181 NMMAFAFHQFTHQFRTDHRKGRPAFTNGIGHGVNDINHLYGETLAROKRLRFKDGKMY 240  
QY 241 QIIDGEMPTVYKDTQAEIMYPPQVPEHLRFAGVGEVFGLVPGIMMYATTIMLRHNRCVD 300  
Db 241 QIIDGEMPTVYKDTQAEIMYPPQVPEHLRFAGVGEVFGLVPGIMMYATTIMLRHNRCVD 300  
QY 301 VLKQHPHMGDQQLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360  
Db 301 VLKQHPHMGDQQLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360  
QY 361 NR1AAEFNTLYMHPLLPDTFOIHQKYNVQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
Db 361 NR1AAEFNTLYMHPLLPDTFOIHQKYNVQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
QY 421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRFLKPYESFEELTGEKMSALELAL 480  
Db 421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRFLKPYESFEELTGEKMSALELAL 480  
QY 481 YGIDAVEVELYPALVLEKPRDAIFGETWVEVGAPELSKGLMGVILCSPAYMKSTGGEV 540  
Db 481 YGIDAVEVELYPALVLEKPRDAIFGETWVEVGAPELSKGLMGVILCSPAYMKSTGGEV 540  
QY 541 GFOINTASTIQLICNNVKGCPFTSPVDPBELIKVTITINASSRSGLDINPTVLKGR 600  
Db 541 GFOINTASTIQLICNNVKGCPFTSPVDPBELIKVTITINASSRSGLDINPTVLKGR 600

## RESULT 10

US-10-260-937-27  
; Sequence 27, Application US/10260937  
; Publication No. US20030220306A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Daniel  
; APPLICANT: Chandrasekharan, N. Vishwanath  
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; PRIOR FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/373,225  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 27  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Oryctolagus cuniculus  
US-10-260-937-27

Query Match 91.8%; Score 2971; DB 15; Length 604;  
Best Local Similarity 89.9%; Pred. No. 1.9e-286;  
Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;

QY 1 MLARALLCAVALASTHAPCCSHPCQNGVCMVSGVDFQYKDCDCTRTGFGNGCSTPEEL 60  
Db 1 MLARALLCAVALASTHAPCCSHPCQNGVCMVSGVDFQYKDCDCTRTGFGNGCSTPEEL 60  
QY 61 TRIKLFLKPTPTVNHILTHFGKFMVNVNIPFLRAIMSIVLTSSHLIDSPPTYNADY 120  
Db 61 TRIKLFLKPTPTVNHILTHFGKFMVNVNIPFLRAIMSIVLTSSHLIDSPPTYNADY 120  
QY 121 GYKSWAFNSLYTRALPVPVDDCPTPLGVKGGKOLPDSNETVEKLLLRKFIIPDQGS 180  
Db 121 GYKSWAFNSLYTRALPVPVDDCPTPLGVKGGKOLPDSNETVEKLLLRKFIIPDQGS 180  
QY 181 NMMAFAFHQFTHQFRTDHRKGRPAFTNGIGHGVNDINHLYGETLAROKRLRFKDGKMY 240  
Db 181 NMMAFAFHQFTHQFRTDHRKGRPAFTNGIGHGVNDINHLYGETLAROKRLRFKDGKMY 240  
QY 241 QIIDGEMPTVYKDTQAEIMYPPQVPEHLRFAGVGEVFGLVPGIMMYATTIMLRHNRCVD 300  
Db 241 QIIDGEMPTVYKDTQAEIMYPPQVPEHLRFAGVGEVFGLVPGIMMYATTIMLRHNRCVD 300  
QY 301 VLKQHPHMGDQQLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360  
Db 301 VLKQHPHMGDQQLFQTSRLILIGETIKIVIEDYVGHLSGYHFKLKFDELLFNKOFOYQ 360  
QY 361 NR1AAEFNTLYMHPLLPDTFOIHQKYNVQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
Db 361 NR1AAEFNTLYMHPLLPDTFOIHQKYNVQOFTYNNSSILLEGITQFVESFTROJAGRY 420  
QY 421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRFLKPYESFEELTGEKMSALELAL 480  
Db 421 AGGRNVPVAVOKVQASIDOSRQMKYQSFNEYKRRFLKPYESFEELTGEKMSALELAL 480  
QY 481 YGIDAVEVELYPALVLEKPRDAIFGETWVEVGAPELSKGLMGVILCSPAYMKSTGGEV 540  
Db 481 YGIDAVEVELYPALVLEKPRDAIFGETWVEVGAPELSKGLMGVILCSPAYMKSTGGEV 540  
QY 541 GFOINTASTIQLICNNVKGCPFTSPVDPBELIKVTITINASSRSGLDINPTVLKGR 600  
Db 541 GFOINTASTIQLICNNVKGCPFTSPVDPBELIKVTITINASSRSGLDINPTVLKGR 600

QY 601 STEL 604  
Db 601 STEL 604

## RESULT 11

US-09-919-060-5  
; Sequence 5, Application US/09919060  
; Patent No. US20020064845A1  
; GENERAL INFORMATION:  
; APPLICANT: Wisniewski, Nancy  
; APPLICANT: Brandt, Kevin S.  
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES  
; FILE REFERENCE: AD-1  
; CURRENT APPLICATION NUMBER: US/09/919,060  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/224,486  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-919-060-5

Query Match 91.7%; Score 2967; DB 9; Length 604;  
Best Local Similarity 90.1%; Pred. No. 4,8e-286;  
Matches 544; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY 1 MLARALLICAVIALSHNTANPCCSHPCQNRGVCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60  
Db 1 MLARALVLCALAVLRANPCCSHPCQNRGVCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60  
QY 61 TRIKFLKPTNTYHYIITTHKGFNNVNNIPLRNALMSYVLSRSHLIDSPPTYNADY 120  
Db 61 TRIKFLKPTNTYHYIITTHKGFNNVNNIPLRNALMSYVLSRSHLIDSPPTYNADY 120  
QY 121 GYKSWAESNLSTYTRALRPVDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180  
Db 121 GYKSWAESNLSTYTRALRPVDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180  
QY 181 NMMEFAFAQHFTHOFFKTDHKGPAFTNGLGHGVDLNIYGETLAROKRLFKDGKKKY 240  
Db 181 NMMEFAFAQHFTHOFFKTDHKGPAFTNGLGHGVDLNIYGETLAROKRLFKDGKKKY 240  
QY 241 QIINGEMVPTVKQTQAMETPRPOVBEHLRPAVGQEVGLVPLMMYATIMLRHNRYCD 300  
Db 241 QIINGEMVPTVKQTQAMETPRPOVBEHLRPAVGQEVGLVPLMMYATIMLRHNRYCD 300  
QY 301 VLKQHPHWDERLFOFTRSLILIGETIKIVIEDVVOHLSGYHFKLPDPELLEPKOFOYQ 360  
Db 301 VLKQHPHWDERLFOFTRSLILIGETIKIVIEDVVOHLSGYHFKLPDPELLEPKOFOYQ 360  
QY 361 NRIAAEFNTLYHMHPLPDTPQIDHOKXNYOQFYNNNSILHEGITQFVESFTROIAGRV 420  
Db 361 NRIAAEFNTLYHMHPLPDTPQIDHOKXNYOQFYNNNSILHEGITQFVESFTROIAGRV 420  
QY 421 AGGNVPRPAVOKVQASIDOSRQMKYOSFNEYRRKFMKPYESBELTGEKEMGALEAL 480  
Db 421 AGGNVPRPAVOKVQASIDOSRQMKYOSFNEYRRKFMKPYESBELTGEKEMGALEAL 480  
QY 481 YGIDDAVELYPALIVEKRPDAIFGETMVEVGAFFSLKGLMGNYICSPAYMKPSTFGGEV 540  
Db 481 YGIDDAVELYPALIVEKRPDAIFGETMVEVGAFFSLKGLMGNYICSPAYMKPSTFGGEV 540  
QY 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELKTVTINASSRSGLDINDINPTVLKER 600  
Db 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELKTVTINASSRSGLDINDINPTVLKER 600  
QY 601 STEL 604  
Db 601 STEL 604

Db 601 STEL 604

## RESULT 12

US-09-949-293-30  
; Sequence 30, Application US/09949293  
; Publication No. US20030082550A1  
; GENERAL INFORMATION:  
; APPLICANT: Thoenen, Hans-Ulrich  
; APPLICANT: Wall, Kristian  
; APPLICANT: Fitzgerald, Michael  
; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE  
; FILE REFERENCE: TECH01-07  
; CURRENT APPLICATION NUMBER: US/09/949,293  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: 60/231,250  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-949-293-30

Query Match 90.8%; Score 2938; DB 10; Length 604;  
Best Local Similarity 88.9%; Pred. No. 3.7e-283;  
Matches 537; Conservative 35; Mismatches 32; Indels 0; Gaps 0;

QY 1 MLARALLICAVIALSHNTANPCCSHPCQNRGVCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60  
Db 1 MLARALVLCALAVLRANPCCSHPCQNRGVCMGVGFQYKDCDCTRTGFGYGCSTPEFL 60  
QY 61 TRIKFLKPTNTYHYIITTHKGFNNVNNIPLRNALMSYVLSRSHLIDSPPTYNADY 120  
Db 61 TRIKFLKPTNTYHYIITTHKGFNNVNNIPLRNALMSYVLSRSHLIDSPPTYNADY 120  
QY 121 GYKSWAESNLSTYTRALRPVDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180  
Db 121 GYKSWAESNLSTYTRALRPVDDCPTPLGVKQKOLPDSNEIYKLLRRKFTIPDDPGS 180  
QY 181 NMMEFAFAQHFTHOFFKTDHKGPAFTNGLGHGVDLNIYGETLAROKRLFKDGKKKY 240  
Db 181 NMMEFAFAQHFTHOFFKTDHKGPAFTNGLGHGVDLNIYGETLAROKRLFKDGKKKY 240  
QY 241 QIINGEMVPTVKQTQAMETPRPOVBEHLRPAVGQEVGLVPLMMYATIMLRHNRYCD 300  
Db 241 QIINGEMVPTVKQTQAMETPRPOVBEHLRPAVGQEVGLVPLMMYATIMLRHNRYCD 300  
QY 301 VLKQHPHWDERLFOFTRSLILIGETIKIVIEDVVOHLSGYHFKLPDPELLEPKOFOYQ 360  
Db 301 VLKQHPHWDERLFOFTRSLILIGETIKIVIEDVVOHLSGYHFKLPDPELLEPKOFOYQ 360  
QY 361 NRIAAEFNTLYHMHPLPDTPQIDHOKXNYOQFYNNNSILHEGITQFVESFTROIAGRV 420  
Db 361 NRIAAEFNTLYHMHPLPDTPQIDHOKXNYOQFYNNNSILHEGITQFVESFTROIAGRV 420  
QY 421 AGGNVPRPAVOKVQASIDOSRQMKYOSFNEYRRKFMKPYESBELTGEKEMGALEAL 480  
Db 421 AGGNVPRPAVOKVQASIDOSRQMKYOSFNEYRRKFMKPYESBELTGEKEMGALEAL 480  
QY 481 YGIDDAVELYPALIVEKRPDAIFGETMVEVGAFFSLKGLMGNYICSPAYMKPSTFGGEV 540  
Db 481 YGIDDAVELYPALIVEKRPDAIFGETMVEVGAFFSLKGLMGNYICSPAYMKPSTFGGEV 540  
QY 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELKTVTINASSRSGLDINDINPTVLKER 600  
Db 541 GFQIINTASIQSLICNNVKGCPFTSFVDPDELKTVTINASSRSGLDINDINPTVLKER 600  
QY 601 STEL 604  
Db 601 STEL 604

RESULT 13  
US-10-260-937-26  
; Sequence 26, Application US/10260937  
; Publication No. US20030220306A1  
; GENERAL INFORMATION:  
; APPLICANT: Chandrasekharan, N. Vishvanath  
; APPLICANT: Simmons, Daniel  
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; CURRENT FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/373,225  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-260-937-26

Query Match 90.8%; Score 2938; DB 15; Length 604;  
Best Local Similarity 88.9%; Pred. No. 3.7e-283;  
Matches 537; Conservative 35; Mismatches 32; Indels 0; Gaps 0;

QY 1 M A R A L L I C A V A L A S H T A N P C C S H P C O N R G V C M S V G F D Y K D C D C R T G F Y G N C S T P E L 60  
DB 1 M A R A L L I C A V A L A S H T A N P C C S H P C O N R G V C M S V G F D Y K D C D C R T G F Y G N C S T P E L 60  
QY 61 T R I K I F L K T P M T V H I L T H F K G F M W N N I P F L R A I N A M S Y V L T S R S H I D S P P T Y N A D Y 120  
DB 61 T R I K I F L K T P M T V H I L T H F K G F M W N N I P F L R A I N A M S Y V L T S R S H I D S P P T Y N A D Y 120  
QY 121 G Y K S W E A F S N L S Y T R A L P P V D D C P T P L G V G K K O L P D S N E I V E K L I R R K F I P D P O G S 180  
DB 121 G Y K S W E A F S N L S Y T R A L P P V D D C P T P L G V G K K O L P D S N E I V E K L I R R K F I P D P O G S 180  
QY 121 G Y K S W E A F S N L S Y T R A L P P V D D C P T P L G V G K K O L P D S N E I V E K L I R R K F I P D P O G S 180  
DB 121 G Y K S W E A F S N L S Y T R A L P P V D D C P T P L G V G K K O L P D S N E I V E K L I R R K F I P D P O G S 180  
QY 181 N M F A F P A Q H F T H O F E K T D H K R G P A F T N G L G H G V D L N H I Y G E T L A R O R K L R L F K D G K M X 240  
DB 181 N M F A F P A Q H F T H O F E K T D H K R G P A F T N G L G H G V D L N H I Y G E T L A R O R K L R L F K D G K M X 240  
QY 241 Q I I D G E M Y P P T Y K D T O A E M I T P P O V P E H L R F A V G E V F G L V P G L M M Y A T T I W L R E H N R V C D 300  
DB 241 Q I I D G E M Y P P T Y K D T O A E M I T P P O V P E H L R F A V G E V F G L V P G L M M Y A T T I W L R E H N R V C D 300  
QY 301 V L K O E H P E M G D E Q L P O T S R L I I G E T I K I V I E D Y V O H L S G Y H F K L F P D E L L F N O Q F O Y O 360  
DB 301 V L K O E H P E M G D E Q L P O T S R L I I G E T I K I V I E D Y V O H L S G Y H F K L F P D E L L F N O Q F O Y O 360  
QY 361 N R I A A E F N T L Y H M H P L L P T F O I H D K N Y O O F I Y N N S I L L E H G I T O F Y E S F T R O A G R V 420  
DB 361 N R I A A E F N T L Y H M H P L L P T F O I H D K N Y O O F I Y N N S I L L E H G I T O F Y E S F T R O A G R V 420  
QY 421 A G G R N P P A V O K V S O A S I D O S R O M K Y O S F N E Y R K R F M L K Y S F E E L T G E K E M S A E L E A L 480  
DB 421 A G G R N P P A V O K V S O A S I D O S R O M K Y O S F N E Y R K R F M L K Y S F E E L T G E K E M S A E L E A L 480  
QY 481 Y G D I D A V E L Y P A L L V E K P R P D A I F G E T M Y E V G A F S L K G L M G N V I C S P A Y M K S T G E V 540  
DB 481 Y G D I D A V E L Y P A L L V E K P R P D A I F G E T M Y E V G A F S L K G L M G N V I C S P A Y M K S T G E V 540  
QY 541 G P O I I N T A S I O S L I C N N V G C E P T S F S V P D E L I K T V T I N A S S R S G L D I N P T V L L K E R 600  
DB 541 G P O I I N T A S I O S L I C N N V G C E P T S F S V P D E L I K T V T I N A S S R S G L D I N P T V L L K E R 600

QY 601 S T E L 604  
DB 601 S T E L 604  
RESULT 14  
US-10-260-937-25  
; Sequence 25, Application US/10260937  
; Publication No. US20030220306A1  
; GENERAL INFORMATION:  
; APPLICANT: Chandrasekharan, N. Vishvanath  
; APPLICANT: Simmons, Daniel  
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; CURRENT FILING DATE: 2002-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/373,225  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-10-260-937-25

Query Match 90.3%; Score 2923; DB 15; Length 604;  
Best Local Similarity 88.9%; Pred. No. 1.2e-281;  
Matches 537; Conservative 32; Mismatches 35; Indels 0; Gaps 0;

QY 1 M A R A L L I C A V A L A S H T A N P C C S H P C O N R G V C M S V G F D Y K D C D C R T G F Y G N C S T P E L 60  
DB 1 M A R A L L I C A V A L A S H T A N P C C S H P C O N R G V C M S V G F D Y K D C D C R T G F Y G N C S T P E L 60  
QY 61 T R I K I F L K T P M T V H I L T H F K G F M W N N I P F L R A I N A M S Y V L T S R S H I D S P P T Y N A D Y 120  
DB 61 T R I K I F L K T P M T V H I L T H F K G F M W N N I P F L R A I N A M S Y V L T S R S H I D S P P T Y N A D Y 120  
QY 121 G Y K S W E A F S N L S Y T R A L P P V D D C P T P L G V G K K O L P D S N E I V E K L I R R K F I P D P O G S 180  
DB 121 G Y K S W E A F S N L S Y T R A L P P V D D C P T P L G V G K K O L P D S N E I V E K L I R R K F I P D P O G S 180  
QY 181 N M F A F P A Q H F T H O F E K T D H K R G P A F T N G L G H G V D L N H I Y G E T L A R O R K L R L F K D G K M X 240  
DB 181 N M F A F P A Q H F T H O F E K T D H K R G P A F T N G L G H G V D L N H I Y G E T L A R O R K L R L F K D G K M X 240  
QY 241 Q I I D G E M Y P P T Y K D T O A E M I T P P O V P E H L R F A V G E V F G L V P G L M M Y A T T I W L R E H N R V C D 300  
DB 241 Q I I D G E M Y P P T Y K D T O A E M I T P P O V P E H L R F A V G E V F G L V P G L M M Y A T T I W L R E H N R V C D 300  
QY 301 V L K O E H P E M G D E Q L P O T S R L I I G E T I K I V I E D Y V O H L S G Y H F K L F P D E L L F N O Q F O Y O 360  
DB 301 V L K O E H P E M G D E Q L P O T S R L I I G E T I K I V I E D Y V O H L S G Y H F K L F P D E L L F N O Q F O Y O 360  
QY 361 N R I A A E F N T L Y H M H P L L P T F O I H D K N Y O O F I Y N N S I L L E H G I T O F Y E S F T R O A G R V 420  
DB 361 N R I A A E F N T L Y H M H P L L P T F O I H D K N Y O O F I Y N N S I L L E H G I T O F Y E S F T R O A G R V 420  
QY 421 A G G R N P P A V O K V S O A S I D O S R O M K Y O S F N E Y R K R F M L K Y S F E E L T G E K E M S A E L E A L 480  
DB 421 A G G R N P P A V O K V S O A S I D O S R O M K Y O S F N E Y R K R F M L K Y S F E E L T G E K E M S A E L E A L 480  
QY 481 Y G D I D A V E L Y P A L L V E K P R P D A I F G E T M Y E V G A F S L K G L M G N V I C S P A Y M K S T G E V 540  
DB 481 Y G D I D A V E L Y P A L L V E K P R P D A I F G E T M Y E V G A F S L K G L M G N V I C S P A Y M K S T G E V 540

QY 541 GFOIINTASIOSLCNNVKGCPFTSFVDPDELTKVTINASSSGLDINDPTVLKER 600  
DB 541 GFKIINTASIOSLICSNNVKGCPFTSFVDPDLTKVTINASSSGLDINDPTVLKER 600  
QY 601 STEL 604  
DB 601 STEL 604

DB 541 NTASIOSLICSNNVKGCPFTSFVDPDLTKVTINASSSGLDINDPTVLKERSTEL 599  
Search completed: April 24, 2004, 07:27:00  
J00 time : 75 secs

RESULT 15  
US-09-949-293-31  
; Sequence 31, Application US/09949293  
; Publication No. US20030082550A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomann, Hans-Ulrich  
; APPLICANT: Wall, Kristian  
; APPLICANT: Fitzgerald, Michael  
; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE  
; FILE REFERENCE: TECH01-07  
; CURRENT APPLICATION NUMBER: US/09/949,293  
; PRIORITY FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: 60/231,250  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-949-293-31

Query Match 89.7%; Score 2902; DB 10; Length 599;  
Best local Similarity 88.8%; Pred. No. 1.4e-279;  
Matches 532; Conservative 32; Mismatches 35; Indels 0; Gaps 0;

QY 6 LILCAVALSHSTANPCGSHPCONRGVMSVGFQYKCDCTRTGFGENCSPTPELTRIKL 65  
DB 1 MILCAVALSGANPCGSHPCONRGVMSVGFQYKCDCTRTGFGENCSPTPELTRIKL 60  
QY 66 FLKPTNTVHYILTFKGFVNVVNNIPFLRNALMSVYLTSSHLIDSPPTNADYGYKSW 125  
DB 61 LLKPTNTVHYILTFKGFVNVVNNIPFLRNALMSVYLTSSHLIDSPPTNADYGYKSW 120  
QY 126 EAFNSLSYTRALPPVPDDCPTPLGVKGGKOLPDSNETIVEKILLRRKFIIPDQGSNMFA 185  
DB 121 EAFNSLSYTRALPPVPDDCPTPLGVKGGKOLPDSNETIVEKILLRRKFIIPDQGSNMFA 180  
QY 186 FFAQHTFQFPTKTHKRGAPFTNGLGHGVDLNHYGETLAROKRLFKDGKMYQITDG 245  
DB 181 FFAQHTFQFPTKTHKRGAPFTNGLGHGVDLNHYGETLAROKRLFKDGKMYQITDG 240  
QY 246 EMYPPTVKDTQAEIYPPQVEHLRFAGQEVFGLVPGIAMYATITWLREHNRVCDVLKOE 305  
DB 241 EMYPPTVKDTQAEIYPPQVEHLRFAGQEVFGLVPGIAMYATITWLREHNRVCDVLKOE 300  
QY 306 HPBWGDEQLFQTSRLILIGETIKIVIEDYVOHLSGYHFKLKPDELLFNKQFOYQNR1AA 365  
DB 301 HPBWGDEQLFQTSRLILIGETIKIVIEDYVOHLSGYHFKLKPDELLFNKQFOYQNR1AA 360  
QY 366 EFNLTLYMHPLLPPTFOIHDQKYNVQOFTYNNSTILLEGITOQVFSPTROIAGRVAGGRN 425  
DB 361 EFNLTLYMHPLLPPTFOIHDQKYNVQOFTYNNSTILLEGITOQVFSPTROIAGRVAGGRN 420  
QY 426 VPPAVQKVSQASIDQSRQMKYQSFNEYKRPMLKPYESFEELTGEKEMAELEALYGDID 485  
DB 421 VPPAVQKVSQASIDQSRQMKYQSFNEYKRPMLKPYESFEELTGEKEMAELEALYGDID 480  
QY 486 AVELYPALLVKRPDAIFGETMVEVGAAPSLSKGLMGANVICSPAYMKRSTFGSEVGFQII 545  
DB 481 AVELYPALLVKRPDAIFGETMVEVGAAPSLSKGLMGANVICSPAYMKRSTFGSEVGFQII 540  
QY 546 NTASIOSLICSNNVKGCPFTSFVDPDELTKVTINASSSGLDINDPTVLKERSTEL 604

Blank

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 24, 2004, 06:44:08 ; Search time 27 Seconds

(without alignments)  
2151.840 Million cell updates/sec

Title: US-08-064-271-10

Perfect score: 3237

Sequence: 1 MIAKALLICAVIALSHNP.....RSGLDINPTVILKERSTEL 604

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3230	99.8	604	2	A46150
2	2881.5	89.0	603	2	JC5063
3	2877	88.9	604	2	A49010
4	2868	88.6	604	2	JC2030
5	2726.5	84.2	603	2	A18630
6	2037	62.9	599	2	UH0259
7	2036.5	62.9	602	2	SE9198
8	2027.5	62.6	602	2	A35564
9	2026.5	62.6	602	2	A39782
10	2017.5	62.3	599	2	A29947
11	2004.5	61.9	600	2	S00561
12	1934.5	59.8	600	2	A28960
13	292	9.0	643	2	T03631
14	268.5	8.3	1475	2	T29809
15	250.5	7.3	1475	2	H96763
16	236	7.7	1506	2	T32909
17	231	7.1	977	2	T16232
18	228.5	7.1	739	2	T29407
19	223	6.9	655	2	T22448
20	219	6.8	1490	2	T24502
21	219	6.8	1490	2	T24502
22	212.5	6.6	718	2	T26073
23	204.5	6.3	773	2	D89013
24	204	6.3	818	1	JC4337
25	203	6.3	894	2	PNO667
26	196.5	6.1	1210	2	T29027
27	190	5.9	891	1	D88013
28	190	5.9	891	1	JN0867
29	181.5	5.6	1328	2	T23007

probable peroxidase  
peroxidasein - frui  
myeloperoxidase (E  
peroxidase (EC 1.1  
iodide peroxidase  
related to feebly  
iodide peroxidase  
gene feebly protei  
iodide peroxidase  
iodide peroxidase  
hypothetical prote  
peroxinectin-like  
peroxidase (EC 1.1  
myeloperoxidase (E  
myeloperoxidase (E  
myeloperoxidase (E

30 173.5 5.4 724 2 T27858  
31 172.5 5.3 1535 2 S46224  
32 170 5.3 718 2 S06068  
33 166.5 5.1 690 2 S28222  
34 164.5 5.1 926 1 OEPGIT  
35 163.5 5.1 355 2 T49753  
36 158.5 4.9 933 1 OPHUIT  
37 157 4.9 445 2 S70648  
38 156 4.8 914 1 S07047  
39 155 4.8 914 1 UN0550  
40 150.5 4.6 1015 2 T32186  
41 148.5 4.6 201 2 S53511  
42 146.5 4.5 712 2 JC4935  
43 146 4.5 745 1 OPHUM  
44 146 4.5 825 2 C28894  
45 146 4.5 830 2 B28894

ALIGNMENTS

RESULT 1  
A46150  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) 2 precursor - human  
N:Alternate names: cyclooxygenase-2; prostaglandin G/H synthase 2; prostaglandin H synth  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1993 #sequence revision 18-Nov-1994 #text change 04-Mar-2000  
C:Accession: A46150; S54973; S46595; S66643; A46042; S50182  
R:Hla, T.; Neilson, K.  
Proc. Natl. Acad. Sci. U.S.A. 89, 7384-7388, 1992  
A:Title: Human cyclooxygenase-2 cDNA.  
A:Reference number: A46150; MUID:92366465; PMID:1380156  
A:Accession: A46150  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-604 <HIA>  
A:Cross-references: EMBL:U04636; NID:G181253; PIDN:AAA58433.1; PID:G181254  
A:Experimental source: umbilical vein endothelial cells  
A:Experimental source: umbilical vein endothelial cells  
R:Appleby, S.B.; Ristimaki, A.; Neilson, K.; Narxo, K.; Hla, T.  
Biochem. J. 302, 723-727, 1994  
A:Title: Structure of the human cyclo-oxygenase-2 gene.  
A:Reference number: S54973; MUID:95031910; PMID:7945196  
A:Accession: S54973  
A:Molecule type: DNA  
A:Residues: 1-164, 'E', 166-604 <APP>  
A:Cross-references: EMBL:U04636; NID:G496975; PIDN:AAA57317.1; PID:G496976  
A:Experimental source: tissue placenta; cell-type endothelium  
R:Kosaka, T.; Miyata, A.; Ihara, H.; Hara, S.; Sugimoto, T.; Takeda, O.; Takahashi, E.;  
Eur. J. Biochem. 221, 889-897, 1994  
A:Title: Characterization of the human gene (PTGS2) encoding prostaglandin-endoperoxide  
A:Reference number: S46595; MUID:94237153; PMID:8181472  
A:Accession: S46595  
A:Status: translation not shown  
A:Residues: 1-164, 'E', 166-604 <KOS>  
A:Molecule type: DNA  
A:Residues: 1-164, 'E', 166-604 <KOS>  
A:Cross-references: EMBL:D28235; NID:G505116; PIDN:BA05698.1; PID:G1020089  
A:Experimental source: Japanese peripheral blood  
R:Memmole, L.P.; Liang, H.; Quintavalla, J.C.; Bowen, B.R.; Wasvary, J.; Miller, D.B.;  
FEBS Lett. 371, 315-320, 1995  
A:Title: Comparison of recombinant cyclooxygenase-2 to native isoforms: aspirin labelin  
A:Reference number: S66643; MUID:96031160; PMID:7556619  
A:Accession: S66643  
A:Molecule type: protein  
A:Residues: 18-21 <KEN>  
R:Jones, D.A.; Carlton, D.P.; McIntyre, T.M.; Zimmerman, G.A.; Prescott, S.M.  
J. Biol. Chem. 268, 9049-9054, 1993  
A:Title: Molecular cloning of human prostaglandin endoperoxide synthase type II and dem  
A:Reference number: A46042; MUID:9322069; PMID:8473346  
A:Accession: A46042  
A:Molecule type: mRNA  
A:Residues: 1-164, 'E', 166-437, 'T', 439-604 <JON>  
A:Cross-references: GB:U15326; NID:G291987; PIDN:AAA35803.1; PID:G291988

A:Experimental source: endothelial cells  
 A:Note: sequence extracted from NCBI backbone (NCBIN:129879, NCBI:129881)  
 R:Barnett, J.; Chow, J.; Ives, D.; Chou, M.; Mackenzie, R.; Osen, E.; Nguyen, B.; Tsing  
 Biochim. Biophys. Acta 1209, 130-139, 1994  
 A:Title: Purification, characterization and selective inhibition of human prostaglandin  
 A:Reference number: S50181; MUID:95035046; PMID:7947975  
 A:Accession: S50182  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-24 <BAR>  
 C:Comment: The active site Ser-516 is predicted to be inhibited by aspirin acetylation.  
 C:Genetics:  
 A:Gene: GDB:PTGS2  
 A:Cross-references: GDB:134805; OMTM:600262  
 A:Map position: 1q25.2-1q25.3  
 A:Introns: 18/1; 57/1; 105/1; 153/1; 213/3; 241/3; 324/1; 419/3; 469/1  
 C:Function:  
 A:Description: catalyzes the oxidative cyclization by oxygen of arachidonic acid to pro  
 A:Pathway: prostaglandin biosynthesis  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 C:Keywords: chromoprotein; endoplasmic reticulum; glycoprotein; heme; iron; metalloprote  
 F:1-17/Domains: signal sequence #status predicted <SIG>  
 F:18-604/Product: prostaglandin-endoperoxide synthase 2 #status experimental <MAT>  
 F:22-54/Domains: EGF homology <EGF>  
 F:130-336/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:295/Binding site: heme iron (His) (axial ligand) #status predicted  
 F:371,516/Active site: Tyr, Ser #status predicted

Query Match 99.8%; Score 3230; DB 2; Length 604;  
 Best Local Similarity 99.8%; Pred. No. 2e-238;  
 Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MLARALLICAVIALSHTANPCCSHPCQNRGVMSVGFQYKDCDCTRTGYGNCSTPEFL 60
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DB 61 TRIKFLKPTPTVYIILTHFGKFNWVNNIPEFLNAINSVYLTSRSHLIDSPPTYNADY 120
QY 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 180
DB 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 180
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DB 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 180
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DB 181 NMMPAFPAQHFTQFFKTDHKGPAFTNGLGHVLDNIHYGETLARQRLRLFKDGKMKY 240
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DB 241 OIIDEMVPTVKDQAEIYPPVPEHLRFVAVGQVFGVGLVMVYATIMLRHNRYCD 300
QY 241 OIIDEMVPTVKDQAEIYPPVPEHLRFVAVGQVFGVGLVMVYATIMLRHNRYCD 300
DB 241 OIIDEMVPTVKDQAEIYPPVPEHLRFVAVGQVFGVGLVMVYATIMLRHNRYCD 300
QY 301 VLKQHPHPEWDBQLFQTSRLILIGETIKIVIEDYVQHSYHFKLKPEDELLFNKQFOYQ 360
DB 301 VLKQHPHPEWDBQLFQTSRLILIGETIKIVIEDYVQHSYHFKLKPEDELLFNKQFOYQ 360
QY 301 VLKQHPHPEWDBQLFQTSRLILIGETIKIVIEDYVQHSYHFKLKPEDELLFNKQFOYQ 360
DB 301 VLKQHPHPEWDBQLFQTSRLILIGETIKIVIEDYVQHSYHFKLKPEDELLFNKQFOYQ 360
QY 361 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTROJAGRY 420
DB 361 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTROJAGRY 420
QY 421 AGGRVNPVAVQKVSQASIDQSRQMKQSFNEFRKRPMLKPYSFELITGKMSALEL 480
DB 421 AGGRVNPVAVQKVSQASIDQSRQMKQSFNEFRKRPMLKPYSFELITGKMSALEL 480
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DB 481 YGDIDAVELYPALLVEKPRDAIPGETWVEGAPFSLKLMGNVICSPPAYMKSTFGGEV 540
QY 541 GQOIIINTASIOICNNVKGCPFTSVDPDELIKVTITNASSSGDIDINPTVILKER 600
DB 541 GQOIIINTASIOICNNVKGCPFTSVDPDELIKVTITNASSSGDIDINPTVILKER 600
QY 601 STEL 604

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Db 601 STEL 604

RESULT 2  
 JC5063  
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 2 precursor - sheep  
 N:Alternate names: prostaglandin H synthase 2  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5063; S68339  
 R:Zheng, V.; O'Sullivan, M.; Hussain, H.; Roswit, W.T.; Holtzman, M.J.  
 Biochem. Biophys. Res. Commun. 227, 499-506, 1996  
 A:Title: Molecular cloning, functional expression, and selective regulation of ovine pro  
 A:Reference number: JC5063; MUID:97032794; PMID:8878543  
 A:Contents: tracheal epithelial cells  
 A:Accession: JC5063  
 A:Molecule type: mRNA  
 A:Residues: 1-603 <ZHA>  
 A:Cross-references: GB:U68486; NID:G1703495; PIDN:ANCA8684.1; PID:G1703496  
 R:Johnson, J.L.; Mims, J.; Buckel, S.D.; Dyer, R.D.; Maddipati, K.R.  
 Arch. Biochem. Biophys. 324, 26-34, 1995  
 A:Title: Purification and characterization of prostaglandin H synthase-2 from sheep plac  
 A:Reference number: S68339; MUID:96095685; PMID:7503555  
 A:Accession: S68339  
 A:Molecule type: protein  
 A:Residues: 17-52; 'G', 100, 'K', 102-115; 183-196; 247-252, 'H', 253-255, 'N', 257, 286-306; 444-45/  
 A:Experimental source: placental cotyledons  
 C:Comment: This enzyme mediates constitutive versus inducible prostanoid production.  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 C:Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase  
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 F:21-53/Domains: EGF homology <EGF>  
 F:276-290/Domains: transmembrane #status predicted <TM>  
 F:52,129,395,579/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:370,515/Active site: Tyr, Ser #status predicted  
 F:373/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 89.0%; Score 2881.5; DB 2; Length 603;  
 Best Local Similarity 87.6%; Pred. No. 7.9e-212;  
 Matches 529; Conservative 35; Mismatches 39; Indels 1; Gaps 1;

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DB 1 MLARALLICAVVCG-ANPCCSHPCQNRGVMSVGFQYKDCDCTRTGYGNCSTPEFL 59
QY 61 TRIKFLKPTPTVYIILTHFGKFNWVNNIPEFLNAINSVYLTSRSHLIDSPPTYNADY 120
DB 60 TRIKFLKPTPTVYIILTHFGKFNWVNNIPEFLNAINSVYLTSRSHLIDSPPTYNADY 119
QY 121 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 180
DB 120 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 179
QY 120 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 180
DB 120 GYKSWAENSLSYTRALPVPVDDCPTPLGVKQKQLPDSNEIVKLLRRKFIPDPOGS 179
QY 181 NMMPAFPAQHFTQFFKTDHKGPAFTNGLGHVLDNIHYGETLARQRLRLFKDGKMKY 240
DB 180 NMMPAFPAQHFTQFFKTDHKGPAFTNGLGHVLDNIHYGETLARQRLRLFKDGKMKY 239
QY 241 OIIDEMVPTVKDQAEIYPPVPEHLRFVAVGQVFGVGLVMVYATIMLRHNRYCD 300
DB 240 OIIDEMVPTVKDQAEIYPPVPEHLRFVAVGQVFGVGLVMVYATIMLRHNRYCD 299
QY 301 VLKQHPHPEWDBQLFQTSRLILIGETIKIVIEDYVQHSYHFKLKPEDELLFNKQFOYQ 360
DB 300 VLKQHPHPEWDBQLFQTSRLILIGETIKIVIEDYVQHSYHFKLKPEDELLFNKQFOYQ 359
QY 361 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTROJAGRY 420
DB 360 NRIAAEFNTLYMHMLPPTFQIHDQKYNVQOPIYNNSLILHGTQFVESFTROJAGRY 419
QY 421 AGGRVNPVAVQKVSQASIDQSRQMKQSFNEFRKRPMLKPYSFELITGKMSALEL 480
DB 421 AGGRVNPVAVQKVSQASIDQSRQMKQSFNEFRKRPMLKPYSFELITGKMSALEL 480

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Db 420 AGRNLPAAVEKSKASLSQSRMAYQSNREIKRFLKPYESFEELTGKEMAALEAL 479  
 QY 481 YGDIDAVELLYPALIVEKRPDAIFGETWVEGAPFSLKGLMGVICSAPYMKPSTFGGEV 540  
 Db 480 YGDIDAMELYPALIVEKRPDAIFGETWVEGAPFSLKGLMGVICSAPYMKPSTFGGEV 539  
 QY 541 GQIINTASTISLISLNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKER 600  
 Db 540 GKRIINTASTISLISLNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKER 599  
 QY 601 STEL 604  
 Db 600 STEL 603

RESULT 3  
 A:Accession: A49010  
 prostaglandin-endoperoxide synthase (EC 1.14.99.1), glucocorticoid-sensitive - mouse  
 N:Alternate names: prostaglandin G/H synthase; prostaglandin synthase/cyclooxygenase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Jan-1994 #sequence revision 18-Nov-1994 #text\_change 17-Nov-2000  
 C:Accession: A49010; A45379; A39854; A41583  
 R:Rybeck, R.P.; Raynoschek, C.; Macdonald-Bravo, H.; Dorfman, K.; Mattei, M.G.; Bravo, R.  
 Cell Growth Differ. 3: 443-450, 1992  
 A>Title: Identification of an immediate early gene, pgs-B, whose protein product has pr  
 A:Reference number: A49010; MUID:93041378; PMID:1419907  
 A:Accession: A49010  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-604 <RVS>  
 A:Experimental source: NIH 3T3 cells  
 A>Note: sequence extracted from NCBI backbone (NCBI:117105)  
 R:O'Banion, M.K.; Winn, V.D.; Young, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 4888-4892, 1992  
 A>Title: cDNA cloning and functional activity of a glucocorticoid-regulated inflammatory  
 A:Reference number: A45379; MUID:92279232; PMID:1594589  
 A:Accession: A45379  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-141, 'A', 143-584, 'H', 586-604 <OIB>  
 A:Cross-references: GB:M88242; NID:G193637; PIDN:AAA37740.1; PID:G193638  
 A>Note: sequence extracted from NCBI backbone (NCBI:104202, NCBI:104203)  
 R:Knjuba, D.A.; Fletcher, B.S.; Varnum, B.C.; Lam, R.W.; Herschman, H.R.  
 J. Biol. Chem. 266, 12866-12872, 1991  
 A>Title: TIS10, a phorbol ester tumor promoter-inducible mRNA from Swiss 3T3 cells, enc  
 A:Reference number: A39854; MUID:91302297; PMID:1712772  
 A:Accession: A39854  
 A:Molecule type: mRNA  
 A:Residues: 1-97, 'T', 99-141, 'A', 143-584, 'H', 586-604 <KUJ>  
 A:Cross-references: GB:M64291; NID:G200336; PIDN:AAA39924.1; PID:G200337  
 R:O'Banion, M.K.; Sadowski, H.B.; Winn, V.; Young, D.A.  
 J. Biol. Chem. 266, 23261-23267, 1991  
 A>Title: A serum- and glucocorticoid-regulated 4-kilobase mRNA encodes a cyclooxygenase-  
 A:Reference number: A41583; MUID:92078199; PMID:1744122  
 A:Accession: A41583  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 281-300, 'L', 302-360 <OAB>  
 A:Genetics: TIS10  
 C:Superfamily: human prostaglandin-endoperoxide synthase, EGF homology  
 C:Keywords: oxidoreductase  
 F:21-54/Domain: EGF homology <EGF>

Query Match 88.9%; Score 2877; DB 2; Length 604;  
 Best Local Similarity 86.9%; Pred. No. 1.7e-211;  
 Matches 523; Conservative 39; Mismatches 40; Indels 0; Gaps 0;

QY 1 MLARALLCAVLASHTANPCSHPCNRRGVCMGVGFQYKCDCTRTGFGENGSTEFLL 60  
 Db 1 MLRAVALLCAALGALGQAANPCSNPCNRRGVCMGVGFQYKCDCTRTGFGENGSTEFLL 60  
 QY 61 TRIKLFLKPTPNVHYILTHFGKGMVWVNNIPFLRNALMSYVLTSRSHLIDSPPTNADY 120

Db 61 TRIKLFLKPTPNVHYILTHFGKGMVWVNNIPFLRNALMSYVLTSRSHLIDSPPTNADY 120  
 QY 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVYKQKQLPDSNIEVKLLRRKFIIDPQGS 180  
 Db 121 GYKSWAFAFNSLSYTRALPVPVDDCPTPLGVYKQKQLPDSNIEVKLLRRKFIIDPQGS 180  
 QY 181 NMFAFPAQHFTHQFETKDHKRGPAFTNGLGHGVNLNIYGETLAROKRLRFKQGMKY 240  
 Db 181 NMFAFPAQHFTHQFETKDHKRGPAFTNGLGHGVNLNIYGETLAROKRLRFKQGMKY 240  
 QY 241 QIIDEMPTPTKDTQAEIMTYPOVBEHAFVAGQEVGLVGLMAYATIMLRHNRVCD 300  
 Db 241 QVIGSEVVPPTKDTQVEMITPPIHBNLQRAVQGVGLVGLMAYATIMLRHNRVCD 300  
 QY 301 VLKQHPWBGDQFQTSRLILIGETIKIVIEDVYQHLSGYHFKLPDELLFNQFOFYQ 360  
 Db 301 ILKQHPWBGDQFQTSRLILIGETIKIVIEDVYQHLSGYHFKLPDELLFNQFOFYQ 360  
 QY 361 NRFAEFNTLTHMHPLLPDTQIHDQKNYQOFTNNSTILHEGITTQVSEFTROIAGRV 420  
 Db 361 NRFAEFNTLTHMHPLLPDTQIHDQKNYQOFTNNSTILHEGITTQVSEFTROIAGRV 420  
 QY 421 AGRNVPPAVQKVSQASIDQSRQMKYQSFNEFKRPFMLKPYESFEELTGKEMAALEAL 480  
 Db 421 AGRNVPPAVQKVSQASIDQSRQMKYQSFNEFKRPFMLKPYESFEELTGKEMAALEAL 480  
 QY 481 YGDIDAVELLYPALIVEKRPDAIFGETWVEGAPFSLKGLMGVICSAPYMKPSTFGGEV 540  
 Db 481 YSDIDAMELYPALIVEKRPDAIFGETWVEGAPFSLKGLMGVICSAPYMKPSTFGGEV 540  
 QY 541 GQIINTASTISLISLNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKER 600  
 Db 541 GFKIINTASTISLISLNNVKGCPFTSGVDPDELTKVTINASSSRSGLDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

RESULT 4  
 A:Accession: JC2030  
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 2 precursor - rat  
 N:Alternate names: cyclooxygenase-2  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text\_change 04-Mar-2000  
 C:Accession: JC2030; PC2015; S39783; A42167  
 R:Kennedy, B.P.; Chan, C.C.; Culp, S.A.; Cromlish, W.A.  
 Biochem. Biophys. Res. Commun. 197, 494-500, 1993  
 A>Title: Cloning and expression of rat prostaglandin endoperoxide synthase (cyclooxygen  
 A:Reference number: JC2030; MUID:94092121; PMID:7916614  
 A:Accession: JC2030  
 A:Molecule type: mRNA  
 A:Residues: 1-604 <KEN>  
 A:Cross-references: GB:L25925; NID:G414812; PIDN:AAA16477.1; PID:G414813  
 A:Accession: PC2015  
 A:Molecule type: protein  
 A:Residues: 18-43 <KE2>  
 R:Feng, L.; Sun, W.; Xia, Y.; Tang, W.W.; Chanmugam, P.; Soyoola, E.; Wilson, C.B.; Hwa  
 Arch. Biochem. Biophys. 307, 361-368, 1993  
 A>Title: Cloning two isoforms of rat cyclooxygenase: differential regulation of their e  
 A:Reference number: S39783; MUID:94099619; PMID:8274023  
 A:Accession: S39783  
 A:Molecule type: mRNA  
 A:Residues: 1-10, 'CPG', 14-57, 'R', 59-65, 'E', 67-95, 'IQS', 99-338, 'R', 340-343, 'Q', 345-349, '  
 A:Cross-references: GB:S67722; NID:G460557; PIDN:AAA29401.1; PID:G460558  
 R:Strohs, J.; Richards, J.S.  
 J. Biol. Chem. 267, 6382-6388, 1992  
 A>Title: Purification and characterization of a novel, distinct isoform of prostaglandin

A:Reference number: A42167; MUID:92210620; PMID:1556140  
 A:Accession: A42167  
 A>Status: preliminary

A: Molecule type protein  
A: Residues: 18-43 <STR>  
C: Comment: This protein provides the prostanoids involved in inflammation and mitogenesis.  
C: Comment: The active site Ser-516 is predicted to be inhibited by aspirin acetylation.  
C: Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C: Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase; tra  
F: 1-17/Domain: signal sequence #status predicted <Sig>  
F: 18-604/Product: prostaglandin-endoperoxide synthase #status predicted <MAT>  
F: 122-54/Domain: EGF homology <EGF>  
F: 127-291/Domain: transmembrane #status predicted <TM>  
F: 553,130,336,580/Binding site: carboxylate (Asn) (covalent) #status predicted  
F: 571,516/Active site: Tyr, Ser #status predicted  
F: 374/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 88.6%; Score 2868; DB 2; Length 604;  
Best Local Similarity 86.4%; Pred. No. 8.5e-211;  
Matches 522; Conservative 40; Mismatches 42; Indels 0; Gaps 0;

QY	1	MLAALLICAVLAISHRANPCCHPCONRGVGVSDQYKCDCTRGFGENCSTPEFL	60
Db	1	MLFPAVALLICAAALASHANPCSCNRCGMSIGDYKCDCTRGFGENCSTPEFL	60
QY	61	TRILKLPKPTNTYHYILLTFEKGFMNVNNIPFLRNAMSIVLTSRSHLIDSPPTYADY	120
Db	61	TRILKLPKPTNTYHYILLTFKGYNNIVNNIPFLRNIMRVLTSRSHLIDSPPTYVHY	120
QY	121	GYSKWEAFNSISYVTRALPVVDDCPPLGVYKKKQLPDSNEIVEKLLRRKFLDPQGS	180
Db	121	GYSKWEAFNSISYVTRALPVVDDCPPLGVYKKKQLPDSNEIVEKLLRRKFLDPQGT	180
QY	181	NMMAFPAQHTHQPFTKDHKSGAFNNGSGHGVDLNHYVETLAROKLRLFPDGCKY	240
Db	181	NMMAFPAQHTHQPFTKDHKSGAFNNGSGHGVDLNHYVETLDRQHKRLFPDGCKLY	240
QY	241	QIIDGEMPPVVKTOQAEIYPPQVPEHLRFVAGQGEVGLVPGMLMYATILREHNEVCD	300
Db	241	QVIGSEVPPVVKDQVMDIYPPVPEHLRFVAGQGEVGLVPGMLMYATILREHNEVCD	300
QY	301	VLKQHEPWPGBOLFQTSRLILIGTKIYIVEDYVQHSGHFLLKRPDELLFNKQROYQ	360
Db	301	ILKQHEPWPGBERLFQTSRLILIGETIKIYIEDVQHLSGHFLLKRPDELLFNQOFQYQ	360
QY	361	NRIAEPFTILHMHPLLDPTFOIHQKYNVQOFLYNNISILHEHSITQFVESFTQIAGR	420
Db	361	NRIAEPFTILHMHPLLDPTFNIEQETFPQFLYNNISILHEGLAHVSEFTQIAGR	420
QY	421	AGRWNPVAVKVSQASIDQSRQMKYQSFENRYRRFMLKPYESEELTGEKEMAEELBAL	480
Db	421	AGRWNPVAVQAVAKASIDQSRQMKYQSLNERYRRFSLKPYTSEELTGEKEMAEELKAL	480
QY	481	YGDIDAVELYPALLVEKRPDAISEMVEVGAPESLKGLMGANYCSPAVYKPTPGGEV	540
Db	481	YHDDIMAEVLPALLVEKRPDAIFGEIWEVGAPESLKGLMGNPICSPQYKAPTFGGEV	540
QY	541	GFQIINTASIOSLGNVKGCPFTSFVSYPDELLIKVTIINASSKSGLDIDNPVLLKER	600
Db	541	GFRINTASIOGLGNVKGCPFASFVQDDPQFTKATINASSHSRLDIDNPVLLIKER	600
QY	601	STEL 604	
Db	601	STEL 604	

RESULT 5  
A38630  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - chicken  
C: Species: Gallus gallus (chicken)  
C: Date: 14-Feb-1992 #sequence\_rev15014-1992 #text\_change 21-Jul-2000  
C: Accession: A38630  
R: Xie, W.; Chipman, J.G.; Robertson, D.L.; Erikson, R.L.; Simmons, D.L.  
Proc. Natl. Acad. Sci. U.S.A. 88, 2692-2696, 1991  
A: Title: Expression of a mitogen-responsive gene encoding prostaglandin synthase is regu  
A: Reference number: A38630; MCID: 91187858; PMID: 1849272

A:Accession: A38630  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-603 <XLE>  
 C:Cross-references: GB:M64990; NID:9212620; PUDN:AAA49050.1; PID:9212621  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 C:Keywords: oxidoreductase  
 F:21-54/Domain: EGF homology <EGF>

Query Match 84.2%; Score 2726.5; DB 2; Length 603;  
 Best Local Similarity 81.6%; Pred. No. 5.3e-200;  
 Matches 493; Conservative 56; Mismatches 54; Indels 1; Gaps 1;

QY	1	MLRALLLICAVLAISHTNPPCCSHPCONRGVMSVGFQDYKDCDCTRTGYGENCSTPEFL	60
DB	1	MLLPCLALLAALIAAGHAANPCCSLPCCONRGVMTGTFDECDCTRTGYGENCTPEEF	60
QY	61	TRIKFLKPEPTNYHYILTHFGKFMNVNVIPEFLNMAISVYLTSKSHLIDSPPTNADY	120
DB	61	TWLKILKPEPTNYHYILTHFGKGVNIIINISFLADTINRYVLTSKSHLIDSPPTNSDY	120
QY	121	GYSKNEAFSNLSYYTRALRPVDPDCTPLGVYGGKQLPDSNIVEKLLIRKFTIPDQS	180
DB	121	SYKSNEAFSNLSYYTRSLRPVGHDCPTPMGVGKKELPDSKILVEKFTLLRRKFTIPDQT	180
QY	181	NMMRAFFQNHFTHFQFKTDHKRGPAFTNGLGHGVLDNHIYGETLARQKLRLEFKDGRKY	240
DB	181	NMFFFFQNHFTHFQFKTDHKRGPGFTKAYGHGVLDNHIYGETLEQLKLRLEKDGRLKY	240
QY	241	QIIDGEMVPTVKDIOAKETIPROYBEHLRFAVGOEFGILVPLGMYATITWLRHNRVCD	300
DB	241	QIIDGEMVPTVKDIOAKETIPRPVBEHLQFSVGQVFGILVPLGMYATITWLRHNRVCD	300
QY	301	VLKQHPHPEWDEQLFQTSRLIIGETIKIVIEDYQHLSGYHKLKPEDELLFNKQFOYQ	360
DB	301	VLKQHPHPEWDEQLFQTSRLIIGETIKIVIEDYQHLSGYHKLKPEDELLFNQRFQYQ	360
QY	361	NRIAEFNTLYMHPLPPTFQIHDQKYNVQOFTYNNLSILLEGITQFVESPTROIAGRY	420
DB	361	NRIAEFNTLYMHPLPPTFQIHNEYTFQOFLYNNLSILLEGHSHMWKVSFKQSGARY	420
QY	421	AGGRNVPPAVQVQASIDQSRQKYQSTNEHFKRPMKPYSEFSELTGKENSABEFLAL	480
DB	421	AGGRNVPPAVQVQAAASIDQSRQKRYQSTNEHFKRPMKPYSEFSELTGKEMAAEEL	480
QY	481	YGDIDAVELVPLALVEKRPDAIFGETWVEVGAFSLKGLMGVICSPAYMKSTEGEV	540
DB	481	YGDIDAMELVPLALVEKRPDAIFGETWVEIGAFSLKGLMGVITCSPEYMKSTEGEV	540
QY	541	GFOIINTASIQSLICNNVKGCPFTSPFVDPBELIKITVTINASSRSGLDIDINPTVLKER	600
DB	541	GFEIINTASIQSLICNNVKGCPFTAFVHNPEPTE-ATINVSSTNAMEDINPTLLKEQ	599
QY	601	STEL 604	
DB	600	SAEL 603	

RESULT 6  
 JH0259  
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 precursor - human  
 N:Alternate names: cyclooxygenase; prostaglandin G/H synthase; prostaglandin H synthase 1  
 N:Contains: prostaglandin-endoperoxide synthase 1, splice form 2  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 04-Mar-2000  
 C:Accession: JH0259; NM0225; A39337; B38146; A38146; S50181; A36746; S69169  
 R:Rakhaishi, Y.; Ueda, N.; Yoshimoto, T.; Yamamoto, S.; Yokoyama, C.; Miyata, A.; Tanabe, T.  
 Biochem. Biophys. Res. Commun. 182, 433-438, 1992  
 A:Title: Immunodeficiency purification and cDNA cloning of human platelet prostaglandin end  
 A:Reference number: JH0259; M0ID:92134251; PMID:1734857  
 A:Accession: JH0259  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <TAKI>

A:Cross-references: GB:S78220; NID:g243971; PIDN:AA21215.1; PID:g243972  
 A:Accession: PH0225  
 A:Molecule type: protein  
 A:Residues: 24-31 <TAK>  
 R:Funck, C.D.; Funck, L.B.; Kennedy, M.E.; Pong, A.S.; Fitzgerald, G.A.  
 FASEB J. 5, 2304-2312, 1991  
 A:Title: Human platelet/erythrocyte leukemia cell prostaglandin G/H synthase: cDNA cloning,  
 A:Reference number: A39337; MUID:91317397; PMID:1907252  
 A:Accession: A39337  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <FUN>  
 A:Cross-references: GB:M59979; NID:g189886; PIDN:AAA03630.1; PID:g189887  
 R:Diaz, A.; Regnato, A.M.; Jimenez, S.A.  
 J. Biol. Chem. 267, 10816-10822, 1992  
 A:Title: Alternative splicing of human prostaglandin G/H synthase mRNA and evidence of  
 nd tumor necrosis factor alpha.  
 A:Reference number: A38146; MUID:92268138; PMID:1587858  
 A:Accession: B38146  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <DIA>  
 A:Cross-references: GB:S36271; NID:g249625; PIDN:AA22217.1; PID:g249626  
 A:Experimental source: lung fibroblast  
 A:Note: sequence extracted from NCBI backbone (NCBIN:103945, NCBI:103946)  
 A:Accession: A38146  
 A:Molecule type: mRNA  
 A:Residues: 1-395,433-599 <DIA>  
 A:Cross-references: GB:S36219; NID:g249623; PIDN:AA22216.1; PID:g249624  
 A:Experimental source: lung fibroblast  
 A:Note: sequence extracted from NCBI backbone (NCBIN:103825, NCBI:103826)  
 R:Barnett, J.; Chow, J.; Ives, D.; Chiu, M.; Mackenzie, R.; Osen, E.; Nguyen, B.; Tsing  
 Biochem. Biophys. Acta 1209, 130-139, 1994  
 A:Title: Purification, characterization and selective inhibition of human prostaglandin  
 A:Reference number: S50181; MUID:95035046; PMID:7947975  
 A:Accession: S50181  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 24-32 <BAR>  
 R:Yokoyama, C.; Tanabe, T.  
 Biochem. Biophys. Res. Commun. 165, 888-894, 1989  
 A:Title: Cloning of human gene encoding prostaglandin endoperoxide synthase and primary  
 A:Reference number: A36746; MUID:90088508; PMID:2512924  
 A:Accession: A36746  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-11, 'L', 13-112, 'L', 114-377, 'T', 379-599 <YOK>  
 A:Cross-references: GB:M31822; NID:g189898; PIDN:AAA6439.1; PID:g387018  
 R:Ren, Y.; Loose-Mitchell, D.S.; Kulmacz, R.J.  
 Arch. Biochem. Biophys. 316, 751-757, 1995  
 A:Title: Prostaglandin H synthase-1: evaluation of C-terminus function.  
 A:Reference number: S69169; MUID:95168861; PMID:7864630  
 A:Accession: S69169  
 A:Molecule type: protein  
 A:Residues: 585-599 <REN>  
 C:Genetics:  
 A:Gene: GDB:PTGS1  
 A:Cross-references: GDB:128070; OMIM:176805  
 A:Map position: 9q32-9q33.3  
 C:Function:  
 A:Description: catalyzes the oxidative cyclization by oxygen of arachidonic acid to pro  
 A:Pathway: prostaglandin biosynthesis  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 C:Keywords: alternative splicing; chromoprotein; endoplasmic reticulum; glycoprotein; he  
 F:1-23/Domain: signal sequence #status predicted <IG>  
 F:24-599/Product: prostaglandin-endoperoxide synthase 1 #status experimental <MATI>  
 F:24-35,433-599/Product: prostaglandin-endoperoxide synthase 1 #status predicted  
 F:35-68/Domain: EGF homology <EGF>  
 F:103,143,409/Binding site: carbonylate (Asn) (covalent) #status predicted  
 F:308/Binding site: heme iron (His) (axial ligand) #status predicted  
 F:384,529/Active site: Tyr, Ser #status predicted

Query Match 62.9%; Score 2037; DB 2; Length 599;  
 Best Local Similarity 59.9%; Pred. No. 2,2e-147;  
 Matches 370; Conservative 94; Mismatches 120; Indels 34; Gaps 4;

QY 2 LARALLGAVLAL-----SHTANPCGSHPCQNRGVCMISGDFQYKDCGR 46  
 Db 1 MRSLLRFLRLLPLPVLLADPGAPTPVNCQCYQHOGICVREGLDRYQCDCGR 60  
 QY 47 TGFYENCSTPEFLTRIKLTKPTNTVYILTHKGFNNVNNIPELNAIMSYLTSR 106  
 Db 61 TQSGPNCIRPLMTWIKRSLRPSFTHEFLHGRWMEFV-NATPEIMRLVLTVA 119  
 QY 107 SHLIDSPPTYNADYGYKSMFASNLSSYTRALRPVDDCPPTLVGYKGLPDPSNEIVEK 166  
 Db 120 SMLISPPYNSAHDIYSWESFNSVSYTRILPSVKDPTMGTKGKKQLDAQLAAR 179  
 QY 167 LILRRKFTPDGCGMMFAFFAQHTHOFKFDHKGAFNTGLGHVDLNIYGETLAR 226  
 Db 180 FLRRKFTPDGCGMMFAFFAQHTHOFKISGKMGREFTLALGHVDLNIYGDNLER 239  
 QY 227 QKRLRFPDQKMKYIILIDEMYPPTVKDQEMIRPOVBEHLRFVAGQEVGLVGLMM 286  
 Db 240 QYQLRFPDQKMKYIILIDEMYPPTVKDQEMIRPOVBEHLRFVAGQEVGLVGLMM 299  
 QY 287 YATVLRHNRVCDVLKOEHPWGDQIPTSRLILIGETIKIVIEDVYQHLSGYFKLK 346  
 Db 300 YATVLRHNRVCDVLKOEHPWGDQIPTSRLILIGETIKIVIEDVYQHLSGYFKLK 359  
 QY 347 FDPPELLFKKOFQONRIAEFTNTLYHMHPLPDTQIHDQKYNQOFTYNNSTLLEHGT 406  
 Db 360 FDPPELLFKKOFQONRIAEFTNTLYHMHPLPDTQIHDQKYNQOFTYNNSTLLEHGT 419  
 QY 407 QVESFTROIAGRVAGNRPVAVQVQASIDQSRQKYGSEFNFRKFMKPYESPFE 466  
 Db 420 ALVDAFSQIAGRIGCGNNMHILHVAVDVIREERKLOPFNEYRRKFMKPYESPFE 479  
 QY 467 LTGEKENSABEALYGDIDAVELYPALIVEKRPDPIFGFTWVEGAFPSKGLMGNYIC 526  
 Db 480 LVGEKEMAAEELBYGIDIDALEFYGLILEKCHPMSIRGESMIEIGAFPSKGLMGNYIC 539  
 QY 527 SPAYWKEPTGGEVGFQIINTASIOSLICNNVKGCFEFSVPEBELIKTYTINASSRS 586  
 Db 540 SPAYWKEPTGGEVGFQIINTASIOSLICNNVKGCFEFSVPEBELIKTYTINASSRS 585  
 QY 587 GLDDINPTVLKERSTEL 604  
 Db 586 --QDDGPAV--ERPSTEL 599

RESULT 7  
 prostaglandin G/H synthase 1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 10-Dec-1999  
 A:Accession: S69198; S69199  
 R:Kiltzler, J.W.  
 submitted to the EMBL Data Library, December 1994  
 A:Reference number: S69198  
 A:Accession: S69198  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-602 <KIT>  
 A:Cross-references: EMBL:U18060; NID:g603051; PIDN:AAA85823.1; PID:g603052  
 R:Kiltzler, J.; Hill, E.; Hardman, R.; Reddy, N.; Philpot, R.; Eling, T.E.  
 Arch. Biochem. Biophys. 316, 856-863, 1995  
 A:Title: Analysis and quantitation of splicing variants of the TPA-inducible PGHS-1  
 A:Reference number: S69199; MUID:95168876; PMID:7864644  
 A:Accession: S69199  
 A:Molecule type: mRNA  
 A:Residues: 61-602 <KIT>  
 A:Cross-references: EMBL:U18060  
 A:Note: only a part of the nucleic acid sequence is shown  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 C:Keywords: alternative splicing  
 F:38-71/Domain: EGF homology <EGF>

Query Match 62.9%; Score 2036.5; DB 2; Length 602;  
Best Local Similarity 64.7%; Pred.No.2.5e-147;  
Matches 357; Conservative 90; Mismatches 104; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNRGVCMVGVPDQYKCDCTRTGEGCNSCTEELTRIKLFLKPTNTVHII 78  
Db NPCCYPCQNGQGVCFVRGDLHDYQDCDCTRTGSGPNCCTIPEIWTMLRSSLRSPSPFTNHL 95  
QY 79 THEKGWNVNVIIPILRNAMSVYLSRSHLIDSPRYNADYCYKMEASNSYSYTRLL 138  
Db THGYWIMEEY-NATFIREVIMRLVITVRSNLLSPSPRYNAHDYISWESNSYSYTRIL 154  
QY 139 PVPDPDCCPTELGVKGGKCOLPDSNEIVEKLLRRKFIIPDPGSSNMMEAFPAQHTHFQFKT 198  
Db PVPDPXCPPTMGKRGKKQLPDHLLAQRLLRRREFIPGPGTNVLEAFPAQHTHFQFKT 214  
QY 199 DHKRGPAFTNGLGHVDLNIYGETLARQKRLFKDGKKKTYOIIDGEMTPRYKTOAE 258  
Db 215 SGKMGGEFTALGHVDLGHIDYDLSERQYHLLFKDGKTKYVDLGEVYPPSEVASVL 274  
QY 259 MYPPOVPEHLREAVGQEVFGVLPGMLMAYATMLREHNRVCDAVKOEHPWGEOLFQTS 318  
Db 275 MRPRPQVPEPKQMAVQGEVFGLLPGMLFETIMLRBNRKCDLLKEHPWWDQOLFQTT 334  
QY 319 RLILIGETIKVIYEDVYHLSGYHFKLKEPDELLFNKOYQNRILAAEFTLYHMHPLP 378  
Db 335 RLILIGETIKIIIEYVQHLGSGYFLQKLPDELLFRAQFYRRIRIALEFNLHMHPLP 394  
QY 379 DTRQIHQKKNYQOFTYNNLSLLEHGTITQVESTRTQIARVAGRVPRVAVQKVSQSI 438  
Db 395 DSFOVGQESYQFLENTSMLDYGEALVDASRQARIGGRNFDYHVLHVEDVI 454  
QY 439 DGRQMYQSGFENEKRRFKMLKPYSEFEELTGEEKMSAEILATYGDIDAVEILYALVEKP 498  
Db 455 KESEEMLQGFENKRRKFGKLPTYSFOEPGEKMAAELELDYGDIDALEFYPGLMEKC 514  
QY 499 RPDALFETIWEVGAPSLKGLMGNTVCSPAYKPSFTFGEVGFQIINTASISGLICNNY 558  
Db 515 QPNSLFESEMIEMGAPPSLKLGLNPICSPEYMKPSFTGDDVGENIVNTASLKLVCGLNT 574  
QY 559 KGCPTFSFVDP 570  
Db 575 KTCPTVSRFVDP 586

RESULT 8  
A35564  
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 11-Jan-2000  
C:Accession: A35564  
R:DeWitt, D.L.; El-Harith, E.A.; Kraemer, S.A.; Andrews, M.J.; Yao, E.F.; Armstrong, R.I.;  
J. Biol. Chem. 265, 5192-5198, 1990  
A:Title: The aspirin and heme-binding sites of ovine and murine prostaglandin endoperoxidase  
A:Reference number: A35564; MUID:90203007; PMID:2108169  
A:Accession: A35564  
A:Molecule type: mRNA  
A:Residues: 1-602 <GB>  
C:Cross-references: DBM411; NID:9200302; PID:AAA3913.1; PID:9200303  
C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
C:Keywords: oxidoreductase  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:37-602/Product: prostaglandin-endoperoxide synthase #status predicted <MOT>  
/38-71/Domain: EGF homology <EGF>

	Query Match	59.6%	Score	2027.5	DB	2	Length	602
	Best Local Similarity	65.0%	Pred.	No.	1.2e+146			
	Matches	359	Conservative	86	Mismatches	106	Indels	Gaps
							1,	
Qy								
	19	NPCSSHPONGGVCMSVGFDDYKDCDCTGTGYGNCSPPELTKLEKLPPTNVHIL						78
		. .						
Dd	36	NPCCTYPONGGVCFRFGIDNYQCDCITGTSGPCICTPIELMTWLRNSLRSPSTTHLL						95

QY THEGFNVNANNIPELRNAINMSVYLTSRSHIDSPPTNADVGYSMEAFSMLSYTRAL 138  
 79 THGFWIMEFV-NATFIREVLMRWLVITASNLIIPSEPTNSADHITSWESFSVSYTRIL 154  
 Db 96 THGFWIMEFV-NATFIREVLMRWLVITASNLIIPSEPTNSADHITSWESFSVSYTRIL 154  
 QY 139 PPVDDCPTPLGVGKKOLPDPSNEIVEKLLLRKRTIPDQSNMFAFFAQQHTQFFCT 198  
 Db 155 PSVFKDCPTPGTGGKKOLPDVOLLAQOLLRRRPTPAQGNILILFAFAQHTQFFCT 214  
 QY 199 DHKSGPAFTNLGKGVLDLNHIYGETLARQKRLPKDGMKYQIIDGEMVPTVKDTQAE 258  
 Db 215 SKGMGPGFTKALGHGVLDLGHYYDNLERQYHLRLKDGKAKIQVLDGEVYPPSEVASVL 274  
 QY 259 MIYPPQVPEHLRFVAVNGQEVFGVLVPGILMMYATIMLRBNRVCVILKOEHEWGDQELFQTS 318  
 Db 275 MRYPGVPPEHQMAVNGQEVFGVLPGILPMFTIMLRBNRVCOLLKEHPHTWDEQLFQTT 334  
 QY 319 RLILIGETIKIVIEDYVOHLSGYAFKCLKFPDPLLNKQFOYQNRILAEENTLYHMPILP 378  
 Db 335 RLILIGETIKIVIEEYVOHLSGYFLQTKFPDPLLRPAQFYQNRILAMENNLHYHMPILP 394  
 QY 379 DTFOIHDCKVNVQOFTYNNSTILBHGITOQVFSFTRQIAGRVAGGNVPVAVQVQSQSI 438  
 Db 395 NSFQVQSOEYITEQLENTSMVDYGVIALVDVAFSRQARIGGGRNPFYHVLHVAVDYI 454  
 QY 439 DQSRQMKQSEFENEYKRRFMLKPYESFEELTGEKEMSALEALYGDIDAVELYPALIVEKP 498  
 Db 455 KESRRMRRLQPFNEHYKRRGLKPKYTSFQELTGEKEMAALEELYGDIDALEFYPGLILLEKC 514  
 QY 499 RPDALFETGTVCEVGAPELSIKGLMGVNTCSPAYMKVSTFGEGVFGQILNTASQSLCNV 558  
 Db 515 QPNSTFGESMTIEMGAPFSLKGLGNPICSPEYMKSTFGGDYGFMLNTASLKKVCLNLT 574  
 QY 559 KGCPSTSPSPVD 570  
 Db 575 KTCPIYSFRVPD 586  
 RESULT 9  
 S39782  
 Cyclicoxygenase 1 - rat  
 CSpecies: Rattus norvegicus (Norway rat)  
 CDate: 20-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Dec-1999  
 CAccession: S39782  
 RArch: Biochem. Biophys. 307, 361-368, 1993  
 ATitle: Cloning two isoforms of rat cyclooxygenase: differential regulation of their ex  
 AReference number: S39782; MID:94099619; PMID:8274023  
 AAccession: S39782  
 A:Molecule type: mRNA  
 A:Residues: 1-602 <FEN->  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 F:38-71/Domain: EGF homology <EGF>

Query Match	54.2%	Score	2026.5	DB 2	length	602
Best Local Similarity	62.6%	Pred. No.	1.4e-146			
Matches	354	Conservative	92	Mismatches	104	Indels 1; Gaps 1

  

QY	20	PCCSHPCONRGVOMSVGFDOYKDCDCTRTGPGYGENCSTPEFLIRIKLFLKTEPTVTHAILT	79
Db	37	PCCYFPCQNOQVCVFGFLHDHYOCCDCTRTGSGENCTPELITWLRLRSLSRSPSETHILTT	96
QY	80	HKKGPMNVNNVNIPELRNATMSYVLTGRSHLIDBPPPYTNADYGVKSWAEFNLISYTRALP	139
Db	97	HGWTWIEFY-NATFLREVLMGWVLYTRSNLIISPPTNYNTHDVISMSSEFNSVSYTRILP	155
QY	140	PVVDDCPTPLGVYKGGKKOLPDSNEIVEKLLIRKFTLPDQGSNNMFAFAOHTHQPFKXTD	199
Db	156	SVPKDCPTPMGTGKGGKQLPDHILALORLLIRREFITAPAOGTNYLFAFAOHTHQPFKXTS	215
QY	200	HKRGPAFTNGLGIGVULNHVGETLARORLRLFKQGMKXQIILIDGMYEPTVDTQAE	259
Db	216	TKMGPEFTALGIGVULGHVIGDSLEROYHRLRFKDGKLLKQYVLDGLYPPSVQASAKM	275



QY 439 DQSRQMKYQSFNRYKRPMLKPYESFEELTGKEMSALELXGDIDAVELYPALVYKRP 498  
 Db 453 KESVLRIRQPFNRYKRPMLKPYESFEELTGKEMSALELXGDIDAVELYPALVYKRP 512  
 QY 499 RPDALFGEIWEVAGPFLSKLGMVNVICSPAYWKSTGEGVGOIINTASIOSTICNNV 558  
 Db 513 HPSNIFGSMLEMAQPFSLKGLNPLICSPFVWKAISTGEGVFNLVATLTKLVCLNT 572  
 QY 559 KGCPFTSVPDP 571  
 Db 573 KTCFVVSFHVDP 585

## RESULT 12

A28960  
 prostaglandin-endoperoxide synthase (EC 1.14.99.1) G/H precursor - sheep  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 10-Dec-1999  
 C:Accession: A28960  
 R:DeWitt, D.L.; Smith, W.L.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1412-1416, 1988  
 A:Title: Primary structure of prostaglandin G/H synthase from sheep vesicular gland dete  
 A:Reference number: A28960; MUID:88144447; PMID:3125548  
 A:Accession: A28960  
 A:Molecule type: mRNA  
 A:Residues: 1-600 <DEW>  
 A:Cross-references: GB:J03599; NID:G166035; PIDN:AAA31576.1; PID:G166036  
 C:Superfamily: human prostaglandin-endoperoxide synthase; EGF homology  
 C:Keywords: oxidoreductase  
 F:36-69/Domain: EGF homology <EGF>

Query Match 59.8%; Score 1934.5; DB 2; Length 600;

Best Local Similarity 62.4%; Pred. No. 1.5e-139; Mismatches 120; Indels 1; Gaps 1;

Matches 345; Conservative 87; Mismatches 120; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNRGCVSVGFDQYKCDCTRTGFEYGCSTPEFLRIKLFLKPTNTVHYIL 78  
 Db 34 NPCCYVPOHQHICVRFGLDRYQCDCTRIAPAPASRRYGPGRGRLCGPAPLSTFVL 93  
 QY 79 THFKGFNVVNNIPFLRNALNSYVLTSHLIDSPPTYADYGYKSWFSLSTYTRAL 138  
 Db 94 THGRMLMPFV-NATFIRDTLMRLVLTVRSNLIPSPPTYADYLSWESFVSSTYTRIL 152  
 QY 139 PVPDPDCPLPLGVKGGKOLPDSNEIYKLLRRKFIPDQGSNMFAFAQHTFOFXT 198  
 Db 133 PVPDPDCPLPLGVKGGKOLPDAEFLSRRLRRKFIPDQGSNMFAFAQHTFOFXT 212  
 QY 199 DHKRGPAFTNGLGHVDLNIHIGETLARQKLRFKDGKMKYQIIDEMYPTVKDTQAE 258  
 Db 213 SKMGSGFTRKALGHVDLGHVIGDNLERQYQLRFKDGKMKYQIIDEMYPTVKDTQAE 272  
 QY 259 MYPPPOVPHLRFANGQEVFGLVPGIMATYMLRHNVCVQLQEHENKMDQLOFQTS 318  
 Db 273 MYPPPOVPHLRFANGQEVFGLVPGIMATYMLRHNVCVQLQEHENKMDQLOFQTS 332  
 QY 319 RLILIGETIKIYEDVVOHLSGHPFLKFPDPELLEFKQFOYONRIAAEENTLYHMHPLP 378  
 Db 333 RLILIGETIKIYEEVVOHLSGHPFLKFPDPELLEFKQFOYONRIAAEENTLYHMHPLP 392  
 QY 379 DTFQIHDQKYNQOFTYNSILHIGITQFVSEFTFQIAGRVAGGNVPAVQVQSASI 438  
 Db 399 DTFQIHDQKYNQOFTYNSILHIGITQFVSEFTFQIAGRVAGGNVPAVQVQSASI 452  
 QY 439 DQSRQMKYQSFNRYKRPMLKPYESFEELTGKEMSALELXGDIDAVELYPALVYKRP 498  
 Db 453 KESVLRIRQPFNRYKRPMLKPYESFEELTGKEMSALELXGDIDAVELYPALVYKRP 512  
 QY 499 RPDALFGEIWEVAGPFLSKLGMVNVICSPAYWKSTGEGVGOIINTASIOSTICNNV 558  
 Db 513 HPSNIFGSMLEMAQPFSLKGLNPLICSPFVWKAISTGEGVFNLVATLTKLVCLNT 572  
 QY 559 KGCPFTSVPDP 571

Db 573 KTCFVVSFHVDP 585

## RESULT 13

103631

oxygenase, pathogen-induced - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999

C:Accession: T03631

R:Sanz, A.; Moreno, J.I.; Castresana, C.

submitted to the EMBL Data Library, July 1998

A:Description: PLOX, a new pathogen-induced oxygenase with homology to animal cyclooxygen

A:Reference number: 214980

A:Accession: T03631

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-643 <SAN>

A:Cross-references: EMBL:AJ007630; NID:e318722; PID:e318723

A:Experimental source: cultivar petite Havana SRI

C:Genetics:

A:Gene: plox

Query Match 9.0%; Score 292; DB 2; Length 643;

Best Local Similarity 21.4%; Pred. No. 3.8e-14; Mismatches 127; Conservative 78; Mismatches 192; Indels 196; Gaps 19;

QY 65 LFLKPTNTVH-----YILTHFKGFNVVNNIPFLRNALNSYVLTSHLIDSPPTYADYGYKSWFSLSTYTRALPVP 107  
 Db 11 LILSPLRPFHFKHDLHIERMTLSKLLFLVHLVDKLNMRPLVLLGLL---YLGAR 67  
 QY 108 HLIDSPPTYN-----ADYKSWF-----AFSNLSYTRALPVP 142  
 Db 68 HLHGE---YNLINVGKTPIGVRSNPDHRYTADKYNDDPENEGAGSELSFGRNMLVD 124  
 QY 143 DDCEPLPLGVKGGKOLPDSNEIYKLLRRKFIPDQGSNMFAFAQHTFOFXT 193  
 Db 125 Q-----HNLKRPDMVAVATKLLARNFVDTSKQFMTAAVIOFMHIDHLEDT 176  
 QY 194 -----OFFKTHKRGPAFTNGLGH-----GVDLNIHIGETLARQ 227  
 Db 177 KOELKAAEVAASQCEPLSFPRFKTELPTGVEYELKTHLNTPTPMWGSALYGSNAEVL 236  
 QY 228 RLRLFLKDGKMKYQI-----ID--GEYTPYVKDTQAEKITPPQVBEHFRVAGQEVRL 280  
 Db 237 KVRFTFKDGKMLKLSADGLLEIDKNGKITISGVRNWA----- 273  
 QY 281 VPGIMATYMLRHNVCVQLQEHENKMDQLOFQTSRLILIGETIKIYEDVVOHLSG 340  
 Db 274 --GLSALQALFVQEHNSVCDALKKEYPLEBEDLYRHARLVSAVIATKHTIDWYEL-- 329  
 QY 341 YHFKLFPDEL-----LFNKQFO-----YONRIAAEF 367  
 Db 330 ----LKTDTLAGMANVYGLLGGKFPDPELLEFKQFOYONRIAAEENTLYHMHPLP 385  
 QY 368 NTLYHMHPLPDTFOIHQDNK---YQOFTYNSILHIGITQFVSEFTFQIAGRVAGGNVPAVQVQSASI 411  
 Db 386 TSVYRHHQDLPLPKQLRINDATPGPKSLPLTNEPLLEDLIGKGGKMLSKIGTKQWVS 445  
 QY 412 FTRQIAGRV-----AGRNVPAPAVQVQSASIDQSRQMKYQSFNRYKRP 455  
 Db 446 MGHQAGALNELNYPVMMRDLPDQVDTGDRPDHD--LAALITYRDRSVAHYRFRG 504  
 QY 456 FMLKPYESFEELTGKEMSALELXGDIDAVELYPALVYKRP 498  
 Db 505 MGIPIKMKEDLTDDDEVINTLGEVYGDVEELDMVGAARLKIYKFAISRT 557

## RESULT 14

T29809

hypothetical protein C46A5.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T29809

[illegible]

B/ANK



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 24, 2004, 04:53:43 ; Search time 18 Seconds  
(without alignments)  
1747.243 Million cell updates/sec

Title: US-08-064-271-10  
Perfect score: 3237  
Sequence: 1 MRAALLCVALSHSTNP.....RSLDINPTVLKERSTEL 604

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3237	100.0	604	1 PGH2_HUMAN	P35554 homo sapien
2	2971	91.8	604	1 PGH2_RABIT	O02768 oryctolagus
3	2938	90.8	604	1 PGH2_HORSE	O19183 equus cabal
4	2923	90.3	604	1 PGH2_BOVIN	O62698 bos taurus
5	2892	89.3	604	1 PGH2_CAVPO	P70682 cavia porce
6	2881.5	89.0	603	1 PGH2_SHEEP	P79208 ovis aries
7	2873	88.8	604	1 PGH2_MOUSE	O05769 m prostagla
8	2868	88.6	604	1 PGH2_RAT	P35355 rattus norv
9	2828	87.4	604	1 PGH2_MOUSE	O62725 mustela vis
10	2726.5	84.2	603	1 PGH2_CHICK	P27607 gallus gall
11	2037	62.9	599	1 PGH2_HUMAN	P23219 homo sapien
12	2036.5	62.9	602	1 PGH1_RAT	O63921 rattus norv
13	2027.5	62.6	602	1 PGH1_MOUSE	P22437 mus musculu
14	2016.5	62.3	600	1 PGH1_SHEEP	P05979 ovis aries
15	1004	31.0	259	1 PGH1_BOVIN	O62664 bos taurus
16	300.5	9.3	978	1 LIDS_GAERG	O9us2 gaueunamow
17	170	5.3	718	1 PERM_MOUSE	P11247 mus musculu
18	166.5	5.1	690	1 PERO_DROME	O01603 drosophila
19	164.5	5.1	926	1 PERP_PIG	P09933 sus scrofa
20	158.5	4.9	933	1 PERT_HUMAN	P07202 homo sapien
21	156	4.8	914	1 PERT_RAT	P14650 rattus norv
22	155	4.8	914	1 PERT_MOUSE	P35419 mus musculu
23	149	4.6	933	1 PERT_CANFA	O8hyb7 canis famli
24	146.5	4.5	712	1 PERL_HUMAN	P22079 homo sapien
25	146	4.5	745	1 PERM_HUMAN	P05164 homo sapien
26	125.5	3.9	1363	1 NX1A_CHICK	O9dd40 gallus gall
27	122.5	3.8	882	1 CUBA_BACUH	O86170 bacillus th
28	122.5	3.8	1477	1 NX1A_HUMAN	O9ub1 homo sapien
29	122.5	3.8	1514	1 NX1A_RAT	O63372 rattus norv
30	122.5	3.8	1530	1 NX1A_BOVIN	O28146 bos taurus
31	121.5	3.8	712	1 PERL_BOVIN	P80025 bos taurus
32	118.5	3.7	1287	1 RPO1_POWPV	O9j593 fowlopx vir
33	118	3.6	715	1 PERE_HUMAN	P16768 homo sapien

34	115	3.6	3135	1	S230 PLAFO	O08372 plasmodium
35	113	3.5	886	1	SDP1_HAEIN	P45119 haemophilus
36	110.5	3.4	1529	1	SLR2_HUMAN	O94813 homo sapien
37	109	3.4	2471	1	NTC2_HUMAN	O04721 homo sapien
38	108.5	3.4	674	1	ETP1_MSEPV	O9yvx9 melanoplus
39	108.5	3.4	2165	1	RRPL_HRSVA	P28887 human respi
40	108	3.3	716	1	PERP_MOUSE	P49290 mus musculu
41	107.5	3.3	1541	1	NX3A_HUMAN	O9y4c0 homo sapien
42	107.5	3.3	1578	1	NX3A_RAT	O07310 rattus norv
43	107	3.3	718	1	LSR2_DROME	O24388 drosophila
44	107	3.3	1072	1	HSBR_RAT	P23897 rattus norv
45	105	3.2	570	1	FBP3_STRPU	P49013 strongyloce

## ALIGNMENTS

RESULT 1  
PGH2\_HUMAN STANDARD; PRT; 604 AA.  
ID P35354; O16876;  
AC 01-JUN-1994 (Rel. 29, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Prostaglandin G/H synthase 2 precursor (BC 1.14.99.1) (Cyclooxygenase  
-2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2  
DE synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).  
GN PTGS2 OR COX2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Endothelial cells;  
RX MEDLINE=9332069; PubMed=8473346;  
RA Jones D.A., Carlton D.P., McIntyre T.M., Zimmerman G.A.,  
RA Prescott S.M.;  
RT "Molecular cloning of human prostaglandin endoperoxide synthase type  
RT II and demonstration of expression in response to cytokines";  
RL J. Biol. Chem. 268:9049-9054 (1993).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Endothelial cells;  
RX MEDLINE=92366465; PubMed=1380156;  
RA Hla T., Neilson K.;  
RT "Human cyclooxygenase-2 cDNA";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:7384-7388 (1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Periphera blood;  
RX MEDLINE=94237153; PubMed=8181472;  
RA Kosaka T., Miyata A., Ihara H., Hara S., Sugimoto T., Takeda O.,  
RA Takahashi E.I., Tanabe T.;  
RT "Characterization of the human gene (PTGS2) encoding prostaglandin-  
RT endoperoxide synthase 2";  
RL Eur. J. Biochem. 221:889-897 (1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=95031910; PubMed=7945196;  
RA Appleby S.B., Ristimaki A., Neilson K., Narko K., Hla T.;  
RT "Structure of the human cyclo-oxygenase-2 gene";  
RL Biochem. J. 302:723-727 (1994).  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANTS HIS-228; ALA-428; ALA-511 AND  
RP ARG-587.  
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,  
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
RA Schekwitz W.S., Sherwood J.K., Wiltrik L.A., Nickerson D.A.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBO databases.  
RN [6]  
RP SEQUENCE FROM N.A.

RA Coville G.;  
 RT Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heish F.,  
 RA Datchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Cannici P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences".  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: May have a role as a major mediator of inflammation  
 CC and/or a role for prostanoil signaling in activity-dependent  
 CC plasticity.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 CC H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 CC molecule (By similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 CC arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- INDUCTION: By cytokines and mitogens.  
 CC -1- DISEASE: Likely to play a role in inflammatory diseases such as  
 CC rheumatoid arthritis.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
 CC peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 CC inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L15326; AAA35803.1; -;  
 DR EMBL: M90100; AAA58433.1; -;  
 DR EMBL: D28235; AAA05698.1; -;  
 DR EMBL: U04636; AAA57317.1; -;  
 DR EMBL: AY229989; AA038056.1; -;  
 DR EMBL: AL033533; CAB41240.1; -;  
 DR EMBL: BC013734; AAH13734.1; -;  
 DR PIR: A46150; A46150.  
 DR HSSP: Q05769; 1CVU.  
 DR Genew, HGNC: 9605; PTGS2.  
 DR MIM: 600262; -;  
 DR GO: GO:0005737; C:cytoplasm; TAS.  
 DR GO: GO:0004666; F:prostaglandin-endoperoxide synthase activity; TAS.  
 DR GO: GO:0006928; P:cell motility; TAS.  
 DR GO: GO:0007582; P:physiological processes; TAS.  
 DR GO: GO:0006933; P:prostaglandin metabolism; TAS.  
 DR InterPro: IPR002007; Anm\_peroxidase.  
 DR InterPro: IPR006209; EGF\_like.

DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR Pfam: PF00008; EGF; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS00022; EGF\_1; FALSE NEG.  
 DR PROSITE: PS01186; EGF\_2; FALSE NEG.  
 DR PROSITE: PS50026; EGF\_3; 1.  
 DR PROSITE: PS50292; PEROXIDASE; 1.  
 DR OXIDOREDUCTASE: Dioxygenase; Peroxidase; Glycoprotein;  
 KM Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;  
 KM Polymorphism.  
 FT SIGNAL 1 17  
 FT CHAIN 18 604  
 FT DOMAIN 18 55  
 FT DISULFID 21 32  
 FT DISULFID 26 42  
 FT DISULFID 44 54  
 FT DISULFID 22 145  
 FT DISULFID 555 561  
 FT ACT SITE 193 193  
 FT ACT SITE 371 371  
 FT METAL 374 374  
 FT SITE 516 516  
 FT CARBOHYD 53 53  
 FT CARBOHYD 130 130  
 FT CARBOHYD 396 396  
 FT CARBOHYD 580 580  
 FT VARIANT 1 1  
 FT VARIANT 228 228  
 FT VARIANT 428 428  
 FT VARIANT 488 488  
 FT VARIANT 511 511  
 FT VARIANT 587 587  
 FT CONFLICT 165 165  
 FT CONFLICT 438 438  
 FT SEQUENCE 604 AA; 68996 MM; 72PFD699F6128519 CRG64;  
 Query Match 100.0%; Score 3237; DB 1; Length 604;  
 Best local similarity 100.0%; Pred. No. 3; 9e-245;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARALLCAVVALSTHAPDCGSHPCONRGVCSVGFDOYKCCCTTGFGNGCSTPEFL 60  
 DB 1 MARALLCAVVALSTHAPDCGSHPCONRGVCSVGFDOYKCCCTTGFGNGCSTPEFL 60  
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 DB TRIKFLKPTPTVAVHILTHFKGFVNVVNNIPLRLNAINSVYLTSSSHLIDSPPTVADY 120  
 QY 121 GYKSWAFAFSLTYTALPPVPDCCPTPLGVKSKKQIPDSNIEVKKLLRRKTIPODGS 180  
 DB 121 GYKSWAFAFSLTYTALPPVPDCCPTPLGVKSKKQIPDSNIEVKKLLRRKTIPODGS 180  
 QY 121 GYKSWAFAFSLTYTALPPVPDCCPTPLGVKSKKQIPDSNIEVKKLLRRKTIPODGS 180  
 DB 121 GYKSWAFAFSLTYTALPPVPDCCPTPLGVKSKKQIPDSNIEVKKLLRRKTIPODGS 180  
 QY 181 NMMEFAFAOFTHOFKTHKRGPAFTNGLGHVVDLNHITGETLARQKRLFRDGMKY 240  
 DB 181 NMMEFAFAOFTHOFKTHKRGPAFTNGLGHVVDLNHITGETLARQKRLFRDGMKY 240  
 QY 241 QIIDGEMPTPTVQTOAEMITPPDVEHLRFVAGQEVFGLVPLAMVATITMREHNRVCD 300  
 DB 241 QIIDGEMPTPTVQTOAEMITPPDVEHLRFVAGQEVFGLVPLAMVATITMREHNRVCD 300  
 QY 301 VLKQEHPEWDEDLFQTSRLILIGETIKIVIBDYVQHLGYHFKLKPDPILLFNKQPOYO 360  
 DB 301 VLKQEHPEWDEDLFQTSRLILIGETIKIVIBDYVQHLGYHFKLKPDPILLFNKQPOYO 360

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QY 361 NRIAEFNTLYMHHPILPDTFOIHDKYNYQOFIYNNLSILHEGITOPESTFROJAGRY 420
DB 361 NRIAEFNTLYMHHPILPDTFOIHDKYNYQOFIYNNLSILHEGITOPESTFROJAGRY 420
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DB 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKYEFEEITGKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVKEKRPDAIFGETMVEVGAPEFSLKGLMGVICSPPAWKSTFGGEV 540
DB 481 YGDIIDAVELYPALLVKEKRPDAIFGETMVEVGAPEFSLKGLMGVICSPPAWKSTFGGEV 540
QY 541 GFOIINTVASTQSLICNNVKGCPFTSFVDPPELTKVTYINASSRSGLDINPTVLLKER 600
DB 541 GFOIINTVASTQSLICNNVKGCPFTSFVDPPELTKVTYINASSRSGLDINPTVLLKER 600
QY 601 STEL 604
DB 601 STEL 604

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## RESULT 2

PGH2\_RABIT STANDARD; PRT; 604 AA.

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AC 002/76;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
DE 2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
DE synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
GN PTGS2 OR COX2 OR COX-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=9793071; PubMed=9249588;
RA Guan Y., Chang M., Cho W., Zhang Y., Redha R., Davis L., Chang S.,
RA Dubois R.N., Hao C.M., Breyer M.;
RT "Cloning, expression, and regulation of rabbit cyclooxygenase-2 in
RT renal medullary interstitial cells.";
RT Am. J. Physiol. 273:F18-F26(1997).
RL
CC -1- FUNCTION: May have a role as a major mediator of inflammation
CC and/or a role for prostanoid signaling in activity-dependent
CC plasticity.
CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
CC H2 + A + H(2)O.
CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
CC molecule (By similarity).
CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
CC arachidonate, first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
CC -1- TISSUE SPECIFICITY: Highest expression in kidney and urinary
CC bladder.
CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
CC peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
CC inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
CC
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CC or send an email to license@isb-sib.ch).

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CC EMBL; U97696; AAB71222.1; -.
DR HSP; 005769; 1CVU.
DR InterPro; IPR002007; Anln_peroxidase.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF03098; An_peroxidase; 1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
DR OXidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
FT SIGNAL 1 17
FT CHAIN 18 604
FT DOMAIN 18 55
FT ACT_SITE 193 193
FT ACT_SITE 371 371
FT METAL 374 374
FT SITE 516 516
FT DISULFID 21 32
FT DISULFID 26 42
FT DISULFID 44 54
FT DISULFID 22 145
FT DISULFID 555 561
FT CARBOHYD 53 53
FT CARBOHYD 130 130
FT CARBOHYD 396 396
FT CARBOHYD 580 580
SQ SEQUENCE 604 AA; 69007 MW; C52F9FBC1F493D7 CR664;

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Query Match 91.8%; Score 2971; DB 1; Length 604;  
 Best Local Similarity 89.9%; Pred. No. 2,4e-224;  
 Matches 543; Conservative 35; Mismatches 26; Indels 0; Gaps 0;

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QY 61 TRIKLFLKPTNTVHYILTHFGFNWVNNIIPFLNNAIWSYVLTGRSHLIDSPPTYNADY 120
DB 61 TRIKLFLKPTNTVHYILTHFGFNWVNNIIPFLNNAIWSYVLTGRSHLIDSPPTYNADY 120
QY 121 GYKSEASNSLYTRALPPVDDCPTPLGVKQKQLPDSNEIVEKLLIRKFTPDQGS 180
DB 121 GYKSEASNSLYTRALPPVDDCPTPLGVKQKQLPDSNEIVEKLLIRKFTPDQGS 180
QY 121 NYKSEASNSLYTRALPPVDDCPTPLGVKQKQLPDSNEIVEKLLIRKFTPDQGS 180
DB 121 NYKSEASNSLYTRALPPVDDCPTPLGVKQKQLPDSNEIVEKLLIRKFTPDQGS 180
QY 181 NMMFAFPFQHFTHQFKTDHKGPAFTNGLGHVLDNHYETLARQRKLRFKQGMKY 240
DB 181 NMMFAFPFQHFTHQFKTDHKGPAFTNGLGHVLDNHYETLARQRKLRFKQGMKY 240
QY 241 QIIDEMYPPTVKDQOAEIYPPQVPEHLRFVAVGEVGLVGLMMYATITLREHNRVCD 300
DB 241 QIIDEMYPPTVKDQOAEIYPPQVPEHLRFVAVGEVGLVGLMMYATITLREHNRVCD 300
QY 241 QVIDEYVPTVKDQOAEIYPPQVPEHLRFVAVGEVGLVGLMMYATITLREHNRVCD 300
DB 241 QVIDEYVPTVKDQOAEIYPPQVPEHLRFVAVGEVGLVGLMMYATITLREHNRVCD 300
QY 301 VLKQHPFWGDEQLFQTSRLIIGRTIKIVIEDYQHLSGYHFKLPDELLFNQOFQY 360
DB 301 VLKQHPFWGDEQLFQTSRLIIGRTIKIVIEDYQHLSGYHFKLPDELLFNQOFQY 360
QY 361 NRIAEFNTLYMHHPILPDTFOIHDKYNYQOFIYNNLSILHEGITOPESTFROJAGRY 420
DB 361 NRIAEFNTLYMHHPILPDTFOIHDKYNYQOFIYNNLSILHEGITOPESTFROJAGRY 420
QY 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKYEFEEITGKEMSALEAL 480
DB 421 AGGRNVPPAVQKVSQASIDSRQMKYQSFNEVYKRFMLKYEFEEITGKEMSALEAL 480
QY 481 YGDIIDAVELYPALLVKEKRPDAIFGETMVEVGAPEFSLKGLMGVICSPPAWKSTFGGEV 540
DB 481 YGDIIDAVELYPALLVKEKRPDAIFGETMVEVGAPEFSLKGLMGVICSPPAWKSTFGGEV 540

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QY 541 GFOIINTASTIOSLICNNVGCPTTSVPPDELIKVTYNASSSGGLDINPTVLKER 600  
 Db 541 GFKIVNTASTIOSLICNNVGCPTTSFNVDPDLKVTYNASSSHSLIEDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

RESULT 3  
 PGH2\_HORSE STANDARD; PRT; 604 AA.

AC 019183;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).  
 GN PTGS2 OR COX2.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OC NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98187796; PubMed=9528947;  
 RA Boerboom D., Sirotis U.;  
 RT "Molecular characterization of equine prostaglandin G/H synthase-2 and regulation of its messenger ribonucleic acid in preovulatory follicles";  
 RT Endocrinology 139:1662-1670(1998).  
 CC -1- FUNCTION: May have a role as a major mediator of inflammation and/or a role for prostanoic signaling in activity-dependent plasticity.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per molecule (By similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
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 CC  
 DR EMBL: AF027335; AAC48808.1; -;  
 DR EMBL: AF027334; AAC07911.1; -;  
 DR HSSP: 005769; 3PGH.  
 DR InterPro: IPR002007; Anim\_peroxidase.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR Pfam: PF00008; EGF; 1.  
 DR PRINTS: PRO0457; ANPEROXIDASE.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE: PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE: PS50026; EGF\_3; 1.

DR PROSITE: PS50292; PEROXIDASE 3; 1.  
 KW Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;  
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.  
 FT SIGNAL 1 17  
 FT CHAIN 18 604  
 FT DOMAIN 18 55  
 FT ACT\_SITE 193 193  
 FT ACT\_SITE 371 371  
 FT METAL 374 374  
 FT SITE 516 516  
 FT DISULFID 21 32  
 FT DISULFID 26 42  
 FT DISULFID 44 54  
 FT DISULFID 22 145  
 FT DISULFID 555 561  
 FT CARBOHYD 53 53  
 FT CARBOHYD 130 130  
 FT CARBOHYD 396 396  
 FT CARBOHYD 580 580  
 SQ SEQUENCE 604 AA; 68847 MW; 28792F7EB513068 CRC64;

Query Match 90.8%; Score 2938; DB 1; Length 604;  
 Best Local Similarity 88.9%; Pred. No. 9e-222;  
 Matches 537; Conservative 35; Mismatches 32; Indels 0; Gaps 0;

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 Db 1 MAARALLCVVALAGNAAPCCSNPCONRGVMSVGFQYKDCCTRTGYGNCSTPEFL 60  
 QY 61 TRIKFLKPLPTNVHILTHFKGFMVNNIPLRNAIVSYLTSSHLIDSPPTNADY 120  
 Db 61 TRIKFLKPLPTNVHILTHFKGFMVNNIPLRNAIVSYLTSSHLIDSPPTNADY 120  
 QY 121 GYKSWFAFNSLSTYTBALPPVDDCPTPLGVKSKOLPDSNEIVKLLRRKPIPDQGS 180  
 Db 121 GYKSWFNSLSTYTBALPPVADGCPPLMGVKKELPDSKEIVKLLRRKPIPDQGT 180  
 QY 181 NMMAFAFQHTFHQFKTDHKKRPAFTNGIGHVVDLNIHGETLARQKRLFKDKMKY 240  
 Db 181 NMMAFAFQHTFHQFKTDHKKRPAFTNGIGHVVDLNIHGETLARQKRLFKDKMKY 240  
 QY 241 QIIDGMYPTVADTOAEMITPPQVPEHLRFVAGQEVFGIVPGLMMYATITWLREHNRVCD 300  
 Db 241 QIINGEVIPTVADTOVEMITPPHPIREHLRFVAGQEVFGIVPGLMMYATITWLREHNRVCD 300  
 QY 301 VLKQHPHWGDEQLPQTSRLILIGETIKIVIEDYVQHLSGYHFKLPDELLFNKQFOYQ 360  
 Db 301 VLKQHPHWDEQLPQTSRLILIGETIKIVIEDYVQHLSGYHFKLPDELLFNKQFOYQ 360  
 QY 361 NRIIAEFNLLYHNPPLPTFOIHDQKNYQOITYNNSSILLEGITQFVASFTRQLAGRY 420  
 Db 361 NRIIAEFNLLYHNPPLPTFOIHDQKNYQOITYNNSSILLEGITQFVASFTRQLAGRY 420  
 QY 421 AGGRNVPVAVOKQASIOSROMKYQSFNEYKRFMLKPYSEFEELTGKEMSALEAL 480  
 Db 421 AGGRNVPVAVOKQASIOSROMKYQSFNEYKRFMLKPYSEFEELTGKEMSALEAL 480  
 QY 481 YGDIIDAVELYPALLVEKPPDAIFGETVYEVGAPSLKGLMGNVICSPAYWKPSTGGEV 540  
 Db 481 YGDIIDAMELYPALLVKPPDAIFGETVYELGAPSLKGLMGNVICSPAYWKPSTGGEV 540  
 QY 541 GFOIINTASTIOSLICNNVGCPTTSVPPDELIKVTYNASSSGGLDINPTVLKER 600  
 Db 541 GFKIVNTASTIOSLICNNVGCPTTSFNVDPDLKVTYNASSSHSLIEDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

RESULT 4  
 PGH2\_BOVIN

ID PGH2 BOVIN STANDARD; PRT: 604 AA.  
 AC 062698; 046517; 062665;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase  
 -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2  
 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).  
 GN PGHS2 OR COX2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21141972; PubMed=11207216;  
 RA Liu J., Antaya M., Goff A.K., Boerboom D., Silversides D.W.,  
 RT Lussier J.G., Stros J.;  
 RT "Molecular characterization of bovine prostaglandin G/H synthase-2 and  
 regulation in uterine stromal cells.";  
 RL Biol. Reprod. 64:983-991(2001).  
 RN [2]  
 RP SEQUENCE OF 105-253 FROM N.A.  
 RX MEDLINE=98006431; PubMed=9348209;  
 RA Asselin E., Drolet P., Fortier M.A.;  
 RT "Cellular mechanisms involved during oxytocin-induced prostaglandin  
 F2alpha production in endometrial epithelial cells in vitro: role of  
 cyclooxygenase-2.";  
 RT Endocrinology 138:4798-4805(1997).  
 CC -1- FUNCTION: May have a role as a major mediator of inflammation  
 and/or a role for prostanoid signaling in activity-dependent  
 plasticity.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 molecule (By similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
 peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
 CC -----  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF031698; AAC04702.1; -;  
 DR EMBL; AF031699; AAC28562.1; -;  
 DR EMBL; AF004944; AAC05592.1; -;  
 DR HSSP; Q05769; 1DDX.  
 DR InterPro: IPR002007; Anim\_peroxidase.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam; PF03098; An\_peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR SMART; SM00181; EGF\_1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 KM Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;

KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.  
 FT SIGNAL 1 17  
 FT CHAIN 18 604  
 FT DOMAIN 18 55  
 FT ACT SITE 193 193  
 FT ACT SITE 371 371  
 FT METAL 374 374  
 FT SITE 516 516  
 FT DISULFID 21 32  
 FT DISULFID 26 42  
 FT DISULFID 44 54  
 FT DISULFID 22 145  
 FT DISULFID 555 561  
 FT CONFLICT 6 6  
 FT CONFLICT 111 111  
 FT CONFLICT 458 458  
 SQ SEQUENCE 604 AA; 65163 MW; 16EA2E51D0A01A45 CRC64;

Query Match 90.3%; Score 2923; DB 1; Length 604;  
 Best Local Similarity 88.9%; Pred. No. 1,3e-220; Indels 0; Gaps 0;  
 Matches 537; Conservative 32; Mismatches 35;

QY 1 MLARALLLCVALALSHIANPCSCSHPCQNGVCMGVGFDPYKDCDCTRTGFYGENCSTPEFL 60  
 DB 1 MLARALLLCVAVALSGAANPCSCSHPCQNGVCMGVGFDPYKDCDCTRTGFYGENCSTPEFL 60  
 QY 61 TRIKLFKRTPTVTHYLTHFGFNNVNNIPPLRNALSYVLTSSHLIDSPPTNADY 120  
 DB 61 TRIKLLEKPTVTHYLTHFGKVVNNIVKISFLRMIMRYLTSSHLIESPTNVAY 120  
 QY 121 GYKSWAFSNTSYRRLPVPVDDCPTPLGVGKXQLPSNSIVETLLRKRFPDQGS 180  
 DB 121 SYKSWAFSNTSYRRLPVPVDDCPTPLGVGKRLPSKVKVKKVLLRRFTIPDQGT 180  
 QY 181 NMFAFFAQHFTQPFKTDHKKRPAFTNGLAGVNLNHYGTLAROKLRPKDGMXY 240  
 DB 181 NLMFAFFAQHFTQPFKTDENGPAFTGKKNHGVLDLSHYGSLERQHLRLFKDGMXY 240  
 QY 241 QIIDEMTPPTVKDQAEKTYPPVPEHLRFAVGEVFGVPLGMVATIMLRHNRYCD 300  
 DB 241 QINIGEMTPPTVKDQVEMIVPPHVEHLKFAVGEVFGVPLGMVATIMLRHNRYCD 300  
 QY 301 VLKQHPFPMGBOLEFQTSRLILIGETIKIVIEDVYOHLSGYNFKLKPDELLFNKQFOYQ 360  
 DB 301 VLKQHPFPMGBOLEFQTSRLILIGETIKIVIEDVYOHLSGYNFKLKPDELLFNKQFOYQ 360  
 QY 361 NR1AAEFNTLYHMHPLPDFTFOIHDQKYNQOQFIYNSILLEHGITQFVESFTROLAGRV 420  
 DB 361 NR1AAEFNTLYHMHPLPDFTFOIHDQKYNQOQFIYNSILLEHGITQFVESFTROLAGRV 420  
 QY 421 AGGRNVPAVQVQSGASIDQSRQMKYQSFNERRKRMKPYESESFEELTGKEMSAELAL 480  
 DB 421 AGGRNLPVAVERKVASIDQSRQMKYQSFNERRKRMKPYESESFEELTGKEMSAELAL 480  
 QY 481 YGDIADVELYFALLVEKRPDAIFGETMVEGAPSLGMLGNVCSAYMWPSTFEGEYV 540  
 DB 481 YGDIADMEFYFALLVEKRPDAIFGETMVEGAPSLGMLGNVCSAYMWPSTFEGEYV 540  
 QY 541 GFQIINTASIGSLI CNNVKGCPTFSVSPDELKITYVINASSRSGHDDINPTYLKXR 600  
 DB 541 GFKIINTASIGSLI CNNVKGCPTFSVSPDELKITYVINASSRSGHDDINPTYLKXR 600  
 QY 601 STEL 604  
 DB 601 STEL 604

RESULT 5  
 PGH2 CAVBO  
 ID PGH2 CAVBO STANDARD; PRT: 604 AA.  
 AC P70682;  
 DT 01-NOV-1997 (Rel. 35, Created)



[1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97032794; PubMed=8878543;  
 RA Zhang V., O'Sullivan M., Hussain H., Roswit W.T., Holtzman M.J.;  
 RT "Molecular cloning, functional expression, and selective regulation  
 of ovine prostaglandin H synthase-2";  
 RL Biochem. Biophys. Res. Commun. 227:499-506(1996).  
 CC -1- FUNCTION: May have a role as a major mediator of inflammation  
 and/or a role for prostanoil signaling in actively-dependent  
 plasticity.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 molecule (by similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 arachidonate, first step.  
 CC -1- SUBUNIT: Homodimer (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
 peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL: U68486; AAC48684.1; -.  
 DR PIR: J05063; J05063.  
 DR HSSP: Q05769; 3PGH.  
 DR InterPro: IPR002007; Anim\_peroxidase.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR02016; Peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR Pfam: PF00008; EGF; 1.  
 DR PRINTS: PRO0457; ANPEROXIDASE.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE: PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE: PS50026; EGF\_3; 1.  
 DR PROSITE: PS50292; PEROXIDASE\_3; 1.  
 DR Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;  
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.  
 FT CHAIN 1  
 FT SIGNAL 16  
 FT DOMAIN 17 603  
 FT ACT\_SITE 192 192  
 FT ACT\_SITE 370 370  
 FT METAL 373 373  
 FT SITE 515 515  
 FT DISULFID 20 31  
 FT DISULFID 25 41  
 FT DISULFID 43 53  
 FT DISULFID 21 144  
 FT DISULFID 554 560  
 FT CARBOHYD 52 52  
 FT CARBOHYD 129 129  
 FT CARBOHYD 395 395  
 FT CARBOHYD 579 579  
 FT SEQUENCE 603 AA; 68969 MW; E27FE0549B81C52 CRC64;  
 Query Match 89.0%; Score 2881.5; DB 1; Length 603;  
 Best Local Similarity 87.6%; Pred. No. 2.3e-217;  
 Matches 529; Conservative 35; Mismatches 39; Indels 1; Gaps 1;

QY 1 MLARALLICAVIALSHSTANPCSSHPQONRGVCSVGFQDKDCTGTGEGNCSTPEFL 60  
 Db 1 MLARALLICAAVVCG-AAAPCCSHPCQNGVCSVGFQDKDCTGTGEGNCSTPEFL 59  
 QY 61 TRIKFLKPTPTVHYILTHFGFNVVANNIPFLRNAISYVLTSSSHIDSPTTNAVY 120  
 Db 60 TRIKFLKPTPTVHYILTHFGFNVVANNIPFLRNAISYVLTSSSHIDSPTTNAVY 119  
 QY 121 GYKSWAEFNSLYTRALPPVDDCPTPLGVKQKQLPDSNEIVKLLRRKPIPPQGS 180  
 Db 120 GYKSWAEFNSLYTRALPPVDDCPTPLGVKQKQLPDSNEIVKLLRRKPIPPQGS 179  
 QY 181 NMMFAFPAQHTFOPEKTDHKGPAFTNGLGCVLNLHLYGETLANQRLKLPKQGMKY 240  
 Db 180 NMMFAFPAQHTFOPEKTDHKGPAFTNGLGCVLNLHLYGETLANQRLKLPKQGMKY 239  
 QY 241 QIIDEMYPPIVKDTQAEVIYPPVDEHLRFVAVGQEVFGLVGLMMYATITWIREHNVCD 300  
 Db 240 QIIDEMYPPIVKDTQAEVIYPPVDEHLRFVAVGQEVFGLVGLMMYATITWIREHNVCD 299  
 QY 301 VLKQHPPEWGEOLPQTSRLILIGETIKIVIEDVYQHLGSGYHPKLPDELLFNKQFOYQ 360  
 Db 300 VLKQHPPEWGEOLPQTSRLILIGETIKIVIEDVYQHLGSGYHPKLPDELLFNKQFOYQ 359  
 QY 361 NRIAEFNTLYHMHFLPDTQIHDQKNYQOFTYNNSTLLEHGTQTFVSTFROIAGRV 420  
 Db 360 NRIAEFNTLYHMHFLPDTQIHDQKNYQOFTYNNSTLLEHGTQTFVSTFROIAGRV 419  
 QY 421 AGGRNVPAVQKVSQASIDQSRQKQYQSFNEFKRFLKPYESFELTGEKMSALEAL 480  
 Db 420 AGGRNVPAVQKVSQASIDQSRQKQYQSFNEFKRFLKPYESFELTGEKMSALEAL 479  
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 Db 480 YGDIIDAVELLYPALVKEKRPDAIRGETNVEGAPPSLKLGMGNVICSPAYKPSFTGGEV 539  
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 Db 540 GFQIINTASISLISCNMKGCPFSFSDPELILKTVITNNSSGSGDDINPTVLKXR 599  
 QY 601 STEL 604  
 Db 600 STEL 603  
 RESULT 7  
 PGH2\_MOUSE  
 ID PGH2\_MOUSE STANDARD; PRT; 604 AA.  
 AC Q05769;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase  
 -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2  
 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II) (Glucocorticoid-  
 regulated inflammatory cyclooxygenase) (Grippeins) (TLIS10 protein)  
 DE (Macrophage activation-associated marker protein P71/73) (PBS-2).  
 GN PTGS2 OR COX2 OR COX-2 OR TLIS10 OR PGHS-B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Swiss;  
 RX MEDLINE=91302297; PubMed=1712772;  
 RA Kujubu D.A., Fletcher B.S., Varnum B.C., Lim R.W., Herschman H.R.;  
 RT "TLIS10, a phorbol ester tumor promoter-inducible mRNA from Swiss 3T3  
 cells, encodes a novel prostaglandin synthase/cyclooxygenase  
 homologue".  
 RU J. Biol. Chem. 266:12866-12872(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.





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FT CONFLICT 142 142 A -> R (IN REF. 3)
FT CONFLICT 585 585 H -> R (IN REF. 3)
FT TURN 20 23
FT STRAND 28 29
FT TURN 31 36
FT STRAND 37 38
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FT HELIX 71 78
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FT HELIX 82 83
FT TURN 90 90
FT HELIX 92 107
FT TURN 108 109
FT STRAND 116 117
FT TURN 118 119
FT STRAND 120 120
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FT TURN 131 132
FT STRAND 133 133
FT STRAND 135 136
FT TURN 143 144
FT STRAND 147 147
FT TURN 148 149

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Query Match Best Local Similarity 86.8%; Score 2873; DB 1; Length 604;  
Matches 524; Conservative 39; Mismatches 41; Indels 0; Gaps 0;

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61 TRIKFLKPTNTVHYIILTFKGFANVNNIIFLNNALMSYLLTSRSHLIDSPPTYNADY 120
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121 GYKSWFASNSLYRRALPRVDDCPTPLGVYKQKQLPDSNFTVYKLLRKFETIDPGS 180
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181 NMFAFPAQHFTHFQKTDHKGPAFTNGLGVDLNIYGETLARQKRLFKDGKKY 240
181 NMFAFPAQHFTHFQKTDHKGPAFTNGLGVDLNIYGETLARQKRLFKDGKKY 240
241 QIIGEMVPTVVKDQAEIYPRVPEHLRPAVGQEVGLVPGLMVATIMLRHNRYCD 300
241 QIIGEMVPTVVKDQAEIYPRVPEHLRPAVGQEVGLVPGLMVATIMLRHNRYCD 300
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301 VLKQHPWGDQOLFQTSRLILIGETIIVIEDVYQHLGSHFKLKEPPELLFNKQFOYQ 360
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301 VLKQHPWGDQOLFQTSRLILIGETIIVIEDVYQHLGSHFKLKEPPELLFNKQFOYQ 360
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361 NRISAFTLYHMHPLPDFTFNIEDQESFKQPLNNLSILHEGLITQVESFTQIAGRV 420
421 AGGNVPAVQVQASIDQSRQKQYGFNYRFRKFMKPYESEPBEELTGEKEMAELEAL 480
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421 AGGNVPAVQVQASIDQSRQKQYGFNYRFRKFMKPYESEPBEELTGEKEMAELEAL 480
481 YGDIADVELYPALVPRPDALFGETMVEVGAFFSLKGLMGVYICSPAVWKSTPGGEV 540
481 YGDIADVELYPALVPRPDALFGETMVEVGAFFSLKGLMGVYICSPAVWKSTPGGEV 540
481 YGDIADVELYPALVPRPDALFGETMVEVGAFFSLKGLMGVYICSPAVWKSTPGGEV 540
541 GFQININASTOSLICNNVKGCPFTSVPPELILKYVINASSRSGLDINDPTVLKER 600
541 GFQININASTOSLICNNVKGCPFTSVPPELILKYVINASSRSGLDINDPTVLKER 600
541 GFQININASTOSLICNNVKGCPFTSVPPELILKYVINASSRSGLDINDPTVLKER 600

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QY 601 STEL 604
DB 601 STEL 604

RESULT 8
PGH2 RAT STANDARD; PRT; 604 AA.
AC P3535; 064379;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
-2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
synthase 2) (PGH synthase 2) (PGHS-2) (PHS II).
GN PGH2 OR COX2 OR COX-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94092121; PubMed=7916614;
RA Kennedy B.P., Chan C.C., Culp S.A., Cromlish W.A.;
RT "Cloning and expression of rat prostaglandin endoperoxide synthase
(cyclooxygenase) -2 cDNA.";
RL Biochem. Biophys. Res. Commun. 197;494-500(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93357029; PubMed=8352945;
RA Yamagata K., Andreasson K.I., Kaufmann W.E., Barnes C.A., Worley P.F.;
RT "Expression of a mitogen-inducible cyclooxygenase in brain neurons:
regulation by synaptic activity and glucocorticoids.";
RL Neuron 11;371-386(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wiistar; TISSUE=Intestine;
RX MEDLINE=94262786; PubMed=8203528;
RA Dubois R.N., Tsujii M., Bishop P., Awad J.A., Makita K.,
RA Larnach A.;
RT "Cloning and characterization of a growth factor-inducible
cyclooxygenase gene from rat intestinal epithelial cells.";
RL Am. J. Physiol. 266;G822-G827(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=9409619; PubMed=8274023;
RA Feng L., Sun W., Xia Y., Tang W.W., Channugam P., Soyoola E.,
RA Wilson C.B., Hwang D.;
RT "Cloning two isoforms of rat cyclooxygenase: differential regulation
of their expression.";
RL Arch. Biochem. Biophys. 307;361-368(1993).
CC -1- FUNCTION: May have a role as a major mediator of inflammation
and/or a role for prostanoind signaling in activity-dependent
plasticity.
CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
H2 + A + H(2)O.
CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
molecule (By similarity).
CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
arachidonate; first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
populations of neurons and is enriched in the cortex and
hippocampus.
CC -1- INDUCTION: By cytokines and mitogens.
CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L25925; AAA16477.1; -
DR EMBL: U04300; AAA20246.1; -
DR EMBL: U03389; AAA03466.1; -
DR EMBL: S67722; AAA29401.1; -
DR PIR: JC2030; JC2030.
DR HSSE: Q05769; 3PGH.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR002016; Peroxidase.
DR InterPro: PF03098; An_peroxidase; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
DR PROSITE: PS50292; Peroxidase; Glycoprotein;
KW Oxioreductase; dioxygenase; Peroxidase; Heme; Iron; Signal; Membrane.
KW Prostaglandin biosynthesis;
FT CHAIN 1 17
FT SIGNAL 1 17
FT DOMAIN 18 604
FT ACT_SITE 193 193
FT ACT_SITE 371 371
FT METAL 374 374
FT SITE 516 516
FT DISULFID 21 32
FT DISULFID 26 42
FT DISULFID 44 54
FT DISULFID 22 145
FT DISULFID 555 561
FT CARBOHYD 53 53
FT CARBOHYD 130 130
FT CARBOHYD 396 396
FT CARBOHYD 580 580
FT CARBOHYD 11 13
FT CONFLICT 58 58
FT CONFLICT 66 66
FT CONFLICT 96 98
FT CONFLICT 339 339
FT CONFLICT 344 344
FT CONFLICT 350 350
FT CONFLICT 368 368
FT CONFLICT 573 573
SQ SEQUENCE 604 AA; 69164 MW; 98E418B25D98FF0C CRC64;

Query Match 88.6%; Score 2866; DB 1; Length 604;
Best Local Similarity 86.4%; Pred. No. 2,7e-216;
Matches 522; Conservative 40; Mismatches 42; Indels 0; Gaps 0;

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DB 181 NMFAFAFHHTHGFPTDQKRGFGFRGLGHVDLNVHVGETLDRGKRLFPDGKXKY 240
QY 241 QIDGEMYPPTVKDQTOAMITPPVPEHLRAVQGEVGLVGLMVMATTLREHNRVCD 300
DB 241 QVIGGEVPPPTVKDQTOAMITPPVPEHLRAVQGEVGLVGLMVMATTLREHNRVCD 300
QY 301 VLKQHPMPWGEQGFQTSRLILIGETIVIEDVYQHSYGFHLKPELLEFNKQFYQ 360
DB 301 ILKQHPMPWDEBLFQTSRLILIGETIVIEDVYQHSYGFHLKPELLEFNKQFYQ 360
QY 361 NRIAEFTLYHMHPLLEDTFQIHQKXNYQOFTYNNLSILHEGITQVBSFTROIARV 420
DB 361 NRIASEFTLYHMHPLLEDTFNIEDQETFFQFTLNNLSILHEGIAHFVESFTROIARV 420
QY 421 AGGRVNPVAVQKVASQASTDQSRQMKYQSFNRYRKFMLKPYSEFELGEXKMSAELBAL 480
DB 421 AGGRVNPVAVQKVASQASTDQSRQMKYQSLNEYRKRFSLKPTTSFELGEXKMAELBAL 480
QY 481 YGDDAVELYPALLVEKRPDAIFGETMVEVGAPEFLSLGLMGNTVCSPAYWKSTFGGERV 540
DB 481 YHDDIMELYPALLVEKRPDAIFGETMVEVGAPEFLSLGLMGNTVCSPAYWKSTFGGERV 540
QY 541 GFOIINTASIOSLGNVYKGCPTFSVYDPELITVTITNASSSGDDINPTLTKR 600
DB 541 GFRINTASIOSLGNVYKGCPTFSVYDPELITVTITNASSSGDDINPTLTKR 600
QY 601 STEL 604
DB 601 STEL 604

RESULT 9
PGH2_MUSVI STANDARD; PRT; 604 AA.
ID PGH2_MUSVI
AC 062725;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase
DE 2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2
DE synthase 2) (PcH synthase 2) (PGHS-2) (PHS II).
GN PTGS2 OR COX2.
OS Mus musculus.
OS Mus musculus.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OC NCBI_TaxID=9607;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=98344842; PubMed=9681517;
RA Song J.H., Stroids J., Houde A., Murphy B.D.;
RT "Cloning, developmental expression, and immunohistochemistry of
RT cyclooxygenase 2 in the endometrium during embryo implantation and
RT gestation in the mink (Mustela vison).";
RL Endocrinology 139:3629-3636(1998).
CC -1- FUNCTION: May have a role as a major mediator of inflammation
CC and/or a role for prostanoind signaling in activity-dependent
CC plasticity.
CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
CC H2 + A + H(2)O.
CC -1- COFACTOR: Binds 1 heme B (Iron-protoporphyrin IX) group per
CC molecule (By similarity).
CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from
CC arachidonate, first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.
CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
CC peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-
CC inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Contains 1 EGF-like domain.

```

CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
 CC -----  
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 CC -----  
 DR EMBL: AF047841; AAC05637.1; -.  
 DR HSPB; Q05769; 1CVU.  
 DR InterPro: IPR002007; Anm.peroxidase.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An.peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS50292; PEROXIDASE 3; 1.  
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 DR Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.  
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 FT CHAIN 18 604  
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 FT ACT\_SITE 193 193  
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 DB 421 AGGRNVPVAVQKVSQASIDQSRMRYOSFNEYKRFMLPYESFEETGKESAELEAL 480  
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 QY 541 GFQIINTASIOSLICNNVAGCPFTSPVDPPELKIYNTVITNASSRGLDINPTVLKER 600  
 DB 541 GFQIINTASIOSLICNNVAGCPFTSPVDPPELKIYNTVITNASSRGLDINPTVLKER 600  
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 DB 601 STEL 604  
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 PGH2\_CHICK STANDARD; PRT; 603 AA.  
 AC P27607;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase  
 DE -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2  
 DE synthase 2) (PGHS-2) (PHS II) (Mitogen-inducible  
 DE PGHS).  
 GN PTGS2 OR CEF-147.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 EX MEDLINE=9118758; PubMed=1849272;  
 RA Xie W., Chipman J.G., Robertson D.L., Erikson R.L., Simmons D.L.;  
 RT "Expression of a mitogen-responsive gene encoding prostaglandin  
 RT synthase is regulated by mRNA splicing";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2692-2696(1991).  
 CC -1- FUNCTION: May play an important role in regulating or promoting  
 CC cell proliferation in some normal and neoplastically transformed  
 CC cells.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 CC H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 CC molecule (By similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 CC arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- INDUCTION: By cytokines and mitogens.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxxygenase and as a  
 CC peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 CC inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
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 CC -----  
 DR EMBL: M64990; AAA49050.1; -.  
 DR PIR: A38630; A38630.



RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McKean P.J., McKean K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences".  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: May play an important role in regulating or promoting  
CC cell proliferation in some normal and neoplastically transformed  
CC cells.  
CC -!- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
CC H2 + A + H(2)O.  
CC -!- COFACTOR: Binds heme B (iron-protoporphyrin IX) group per  
CC molecule (by similarity).  
CC -!- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
CC arachidonate; first step.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Membrane-associated. Mitochondrial membrane.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=P23219-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P23219-2; Sequence=VSP\_004673;  
CC -!- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
CC peroxidase.  
CC -!- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
CC inflammatory drugs such as aspirin.  
CC -!- SIMILARITY: Contains 1 EGF-like domain.  
CC -!- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
CC  
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CC DR EMBL; S36219; AAB22216.1; -;  
CC DR EMBL; M59979; AAA03630.1; -;  
CC DR EMBL; S36271; AAB22217.1; -;  
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CC DR EMBL; M31822; AAA36439.1; ALT. SEQ.  
CC DR EMBL; M31812; AAA36439.1; JOINED.  
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CC DR PIR; JH0259; JH0259.  
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CC DR GO; GO:0007582; P:physiological processes; TAS.  
CC DR InterPro; IPR002007; Anim\_peroxidase.  
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CC DR InterPro; IPR02016; Peroxidase.

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KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;  
KW EGF-like domain; Alternative splicing; Polymorphism.  
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QY 107 SHLIDSPPTVADYGYKSWEAFAFNSLYTRALPPVDDCPTPLGVKGGKOLPDSNEIVEK 166  
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QY 167 LLRRKRPDPQGSNNMFAFPAQFTHQFFKTDHKGGAFTNGLGAGVDLNIYGETLAR 226  
DB 180 FLRRKRPDPQGSNNMFAFPAQFTHQFFKTSKMGSGFKALGHVDLNIYGDNLRR 239  
QY 227 QRLRLPFDGKMKQIIGDEMYRPTVKDQAEMLYRQVPHRLRFVAGQEFGLVGLMM 286  
DB 240 QYRLRLKDGKLTQVLDGEMYPSPVSEDAVLMYPRGIPQSGMAVQGFGLPGMLL 299  
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QY 347 FDEPLLNNKQFOYQNRILAAEENLTYLHWPPLIPDTFOIHDQKXNYQPIYNNISLHGIT 406  
DB 360 FDEPLLFGVQFOYQNRILAAEENLTYLHWPPLIPDTFOIHDQKXNYQPIYNNISLHGIT 419

CC 407 QFVESFTQIAGRVAGSNVPPAVQKVSQASIDGRQMKYGFNFYRKRPMIKYESTEE 466  
 CC 420 ALVDAFSSQIAGRIGCGRMDHIIHVADVIRESRMKLOPFNRYRKRFGKPKYTSQOE 479  
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 CC 587 GUDINPYVLKERSTEL 604  
 CC 586 --QDDGPAY--ERPSTEL 599  
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 CC RESULT 12  
 CC PGH1\_RAT STANDARD; PRT; 602 AA.  
 CC ID PGH1\_RAT 063921; Q62731; Q63684;  
 CC AC 15-DEC-1998 (Rel. 37, Last sequence update)  
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 CC DE Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase  
 CC -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2  
 CC synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1).  
 CC GN PTGS1 OR COX1 OR COX-1.  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
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 CC RC STRAIN=Sprague-Dawley;  
 CC RX MEDLINE=94099619; PubMed=8274023;  
 CC RA Feng L., Sun W., Xia Y., Tang W.W., Channugam P., Soyoola E.,  
 CC "Cloning two isoforms of rat cyclooxygenase: differential regulation  
 CC of their expression.";  
 CC Arch. Biochem. Biophys. 307:361-368(1993).  
 CC RL Arch. Biochem. Biophys. 316:856-863(1995).  
 CC RT PGHS-1 mRNA in rat tracheal epithelial cells.";  
 CC "Analysis and quantitation of splicing variants of the TPA-inducible  
 CC cell proliferation in some normal and neoplastically transformed  
 CC cells."  
 CC -1- FUNCTION: May play an important role in regulating or promoting  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 CC H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 CC molecule (By similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 CC arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
 CC peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 CC inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
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 CC CC EMBL; U03388; AAA03465.1; -  
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 CC DR HSSP; P05979; ICOE.  
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 CC DR InterPro; IPR006209; EGF\_Like.  
 CC DR InterPro; IPR006210; IEGF.  
 CC DR InterPro; IPR020106; Peroxidase.  
 CC DR Pfam; PF03098; An\_peroxidase; 1.  
 CC DR PRINTS; PR00457; ANPEROXIDASE.  
 CC DR SMART; SM00181; EGF\_1.  
 CC DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 CC DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 CC DR PROSITE; PS50026; EGF\_3; 1.  
 CC DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 CC DR Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;  
 CC KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;  
 CC EGF-like domain.  
 CC KM  
 CC FT SIGNAL 1 26  
 CC FT CHAIN 27 602  
 CC FT DOMAIN 34 72  
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 CC QY 79 TRKGFPNVNNIPFLNALMSVYLSRSHLIDSPPTYNADYGYKSWAESNLSYTRAL 138  
 CC DB 96 THGYWIEFY-NATFLIREVIMRLVITRSNLISPPPTYNRAHDYISNHSNVSYYRIL 154  
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 CC DB 275 MRYPPGVPEKQMAVGVGEFVLVGLMMVATITWRHNRVQDVYKQHEPENGQQLPOTS 334

QY 319 RLILIGETIKIVIEDVVOHLSGYHFKLKPPELLFNKOFOYQNRNIAEFNTLYHMBLLP 378  
 Db 335 RLILIGETIKIVIEVVOHLSGYFLQKPEDELLFRQOFOYRNRIALFENHLYHMBLLP 394  
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 Db 455 KESREMKLOSFNERYKRFMLKPYTSFOEFTGEKMALEBELYGDIDALFFYGLMLEKC 514  
 QY 499 RPDALFGETMVEVGAPEFLKGMGNVCSAPYKPFSEFGEVGFQIINTASISLCCNNV 558  
 Db 515 QPNSLIGESMIEWGAPEFLKGLGNPCSPYKPFSEFGDVGFINVTASLKKVCLNLT 574  
 QY 559 KGCFTSFSVVD 570  
 Db 575 KTCPVYSFRVVD 586

## RESULT 13

PGH1\_MOUSE STANDARD: PRT; 602 AA.

AC P22437;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase  
 DE -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2  
 GN PTGS1 OR COX1 OR COX-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90203007; PubMed=2108169;  
 RA Dewitt D.L., El-Harich E.A., Kraemer S.A., Andrews M.J., Yao E.F.,  
 RA Armstrong R.L., Smith W.L.;  
 RT "The aspirin and heme-binding sites of ovine and murine prostaglandin  
 RT endoperoxide synthases";  
 RL J. Biol. Chem. 265:5192-5198(1990).  
 CC -1- FUNCTION: May play an important role in regulating or promoting  
 CC cell proliferation in some normal and neoplastically transformed  
 CC cells.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 CC H2 + A + H(2)O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 CC molecule (By similarity).  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 CC arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
 CC peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 CC inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, M4141; AAA39913.1; -.  
 CC DR PIR; A35564; A35564.

DR HSSP; P05979; IDIY.  
 DR MGD; MG1.97797; Ptgs1.  
 DR GO; GO:0005737; C:cytoplasm; IDA.  
 DR GO; GO:0005792; C:mitosome; IDA.  
 DR GO; GO:0001516; P:prostaglandin biosynthesis; IMP.  
 DR GO; GO:0008217; P:regulation of blood pressure; IMP.  
 DR InterPro; IPR006207; Anm peroxidase.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR002016; Peroxidase.  
 DR Pfam; PF03098; An\_peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 DR Oxidoreductase; dioxygenase; Peroxidase; 1.  
 KW Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;  
 KM EGF-like domain.  
 FT SIGNAL 1 26  
 FT CHAIN 27 602  
 FT DOMAIN 34 72  
 FT ACT\_SITE 209 209  
 FT ACT\_SITE 387 387  
 FT METAL 390 390  
 FT SITE 532 532  
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 FT DISULFID 43 59  
 FT DISULFID 61 71  
 FT DISULFID 161 161  
 FT DISULFID 571 577  
 FT CARBOHYD 70 70  
 FT CARBOHYD 106 106  
 FT CARBOHYD 146 146  
 SQ SEQUENCE 602 AA; 69042 MW; 634C0B602045C3A0 CRC64;

Query Match 62.6%; Score 2027.5; DB 1; Length 602;  
 Best Local Similarity 65.0%; Pred. No. 1.3e-150;  
 Matches 359; Conservative 86; Mismatches 106; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNRGVCSVGFDPQKCPRTGFGYGCSPPEFLTKLFLKPTNTVHTL 78  
 Db 36 NPCCYPCQNRGVCSVGFDPQKCPRTGFGYGCSPPEFLTKLFLKPTNTVHTL 95  
 QY 79 THFGFMVNNIIFPLNAINSVYLSRSHLIDSPPTNADYGYKSEAFNLSYTPAL 138  
 Db 96 THGYWMEFV-NATFIREVIMRLVLTWRSNLIISPPTNADYGYKSEAFNLSYTPAL 154  
 QY 139 PPVPDDCPPLGVYGVGKQQLPDSNIEVTKLIRKFTIDPQCSNMFAFAHFTHOPEKT 198  
 Db 155 PSVXKDCPTPMGTGKQQLPDSNIEVTKLIRKFTIDPQCSNMFAFAHFTHOPEKT 214  
 QY 199 DHKRGPAFTNGLSGVVDLNIYGETLARQKRLRFQKQKXKYOUIDEMEPPTKYDQAE 258  
 Db 215 SGKKGPFTFALGHGVDLGHITGDNLERQHLRFLQKQKXKYOUIDEMEPPTKYDQAE 274  
 QY 259 MIYPPQVPEHLRAVGOEVFGLVGLMMVATIMLRHNRCVDVLKQHPMGDEQLPOTS 318  
 Db 275 MRYPPGPVPRQVAVGOEVFGLVGLMMVATIMLRHNRCVDVLKQHPMGDEQLPOTS 334  
 QY 319 RLILIGETIKIVIEDVVOHLSGYHFKLKPPELLFNKOFOYQNRNIAEFNTLYHMBLLP 378  
 Db 335 RLILIGETIKIVIEVVOHLSGYFLQKPEDELLFRQOFOYRNRIALFENHLYHMBLLP 394  
 QY 379 DTFOIHQKXNYQOPIYNNISILHEGITOFEVSEFTROIAGVAGGNVPAPVQVQSASI 438  
 Db 395 DSFGVGSQEXSYEGFLFNTSMVDVYGEVALVDASRQAGRIIGGNRFDYHVLHADV 454  
 QY 439 DOSQOMKXOSFNERYKRFMLKPYESFEBELTGEKMSAELBALYGDIDAVELYPALLVEKP 498  
 Db 455 KESREMKLOSFNERYKRFMLKPYTSFOEFTGEKMALEBELYGDIDALFFYGLMLEKC 514

QY 499 RPDALFETWVEGAPPSLKLGMNVICSPAYKPTSGEVGQIINTASLOSLICNV 558  
 Db 515 QPNSIFGSMTEMGAPFSLKGLNIPICSPYKPTSGEVGQIINTASLKLVCINT 574  
 QY 559 KGCEPTSGSVDP 570  
 Db 575 KTCFVSPRPD 586

RESULT 14  
 PGH1 SHEEP  
 ID PGH1 SHEEP STANDARD; PRT; 600 AA.  
 AC P05379;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 1 precursor (BC 1.14.99.1) (Cyclooxygenase  
 -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2  
 synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1).  
 GN PTHS1 OR COX1.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Vesicular gland;  
 RX MEDLINE=88144447; PubMed=3125548;  
 RA Dewitt D.L., Smith W.L.;  
 RT "Primary structure of prostaglandin G/H synthase from sheep vesicular  
 gland determined from the complementary DNA sequence.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 85:1412-1416(1988).  
 RL (2)  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RP MEDLINE=88196421; PubMed=3129310;  
 RA Yokoyama C., Takai T., Tanabe T.;  
 RT "Primary structure of sheep prostaglandin endoperoxide synthase  
 deduced from cDNA sequence.";  
 RT FEBS Lett. 231:347-351(1988).  
 RL (3)  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=88153641; PubMed=2831188;  
 RA Merlie J.P., Fagan D., Mudd J., Needleman P.;  
 RT "Isolation and characterization of the complementary DNA for sheep  
 semil vesicle prostaglandin endoperoxide synthase  
 (cyclooxygenase).";  
 RT J. Biol. Chem. 263:3550-3553(1988).  
 RL (4)  
 RN SEQUENCE OF 523-544.  
 RP MEDLINE=84024608; PubMed=6414516;  
 RA Roth G.J., Machuga E.T., Ozols J.;  
 RT "Isolation and covalent structure of the aspirin-modified,  
 active-site region of prostaglandin synthetase.";  
 RT Biochemistry 22:4672-4675(1983).  
 RL (5)  
 RN HEME-BINDING SITE.  
 RP MEDLINE=90203007; PubMed=2108169;  
 RA Dewitt D.L., El-Hariri E.A., Kraemer S.A., Andrews M.J., Yao E.F.,  
 RA Armstrong R.L., Smith W.L.;  
 RT "The aspirin and heme-binding sites of ovine and murine prostaglandin  
 endoperoxide synthases.";  
 RT J. Biol. Chem. 265:5192-5198(1990).  
 RL (6)  
 RN ACTIVE SITE TYR-385.  
 RP MEDLINE=91056037; PubMed=2122967;  
 RA Shimokawa T., Kilmacz R.J., Dewitt D.L., Smith W.L.;  
 RT "Tyrosine 385 of prostaglandin endoperoxide synthase is required for  
 cyclooxygenase catalysis.";  
 RT J. Biol. Chem. 265:20073-20076(1990).  
 RL (7)  
 RN CARBOHYDRATE-LINKAGE SITES.  
 RP MEDLINE=93352648; PubMed=8349699;

RA Otto J.C., Dewitt D.L., Smith W.L.;  
 RT "N-glycosylation of prostaglandin endoperoxide synthases-1 and -2 and  
 RT their orientations in the endoplasmic reticulum.";  
 RL J. Biol. Chem. 268:18234-18242(1993).  
 RN (8)  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).  
 RX MEDLINE=94166877; PubMed=8121489;  
 RA Picot D., Loll P.J., Garavito R.M.;  
 RT "The X-ray crystal structure of the membrane protein prostaglandin H2  
 synthase-1.";  
 RL Nature 367:243-249(1994).  
 RN (9)  
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).  
 RX MEDLINE=96022982; PubMed=7552725;  
 RA Loll P.J., Picot D., Garavito R.M.;  
 RT "The structural basis of aspirin activity inferred from the crystal  
 structure of inactivated prostaglandin H2 synthase.";  
 RL Nat. Struct. Biol. 2:637-643(1995).  
 RN (10)  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).  
 RX MEDLINE=96248328; PubMed=8652509;  
 RA Loll P.J., Picot D., Ekabo O., Garavito R.M.;  
 RT "Synthesis and use of iodinated antiinflammatory drug analogs as  
 RT crystallographic probes of the prostaglandin H2 synthase  
 cyclooxygenase active site.";  
 RL Biochemistry 35:7330-7340(1996).  
 RN (11)  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE=20446270; PubMed=10988074;  
 RA Malkowski M.G., Ginell S.L., Smith W.L., Garavito R.M.;  
 RT "The productive conformation of arachidonic acid bound to  
 RT prostaglandin synthase.";  
 RL Science 289:1933-1937(2000).  
 RN (12)  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE=21167849; PubMed=1121413;  
 RA Thureson E.D., Malkowski M.G., Lakkides K.M., Rieke C.J.,  
 RA Mulichak A.M., Ginell S.L., Garavito R.M., Smith W.L.;  
 RT "Mutational and X-ray crystallographic analysis of the interaction of  
 RT dihydro-gamma-linolenic acid with prostaglandin endoperoxide H  
 RT synthase.";  
 RL J. Biol. Chem. 276:10358-10365(2001).  
 RN (13)  
 RP X-RAY CRYSTALLOGRAPHY (2.61 ANGSTROMS).  
 RX MEDLINE=21218593; PubMed=11318639;  
 RA Selinsky B.S., Gupta K., Sharkey C.T., Loll P.J.;  
 RT "Structural analysis of NSAID binding by prostaglandin H2 synthase:  
 RT time-dependent and time-independent inhibitors elicit identical enzyme  
 RT conformations.";  
 RL Biochemistry 40:5172-5180(2001).  
 CC -1- FUNCTION: May play an important role in regulating or promoting  
 CC cell proliferation in some normal and neoplastically transformed  
 CC cells.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 CC H2 + A + H2O.  
 CC -1- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 CC molecule.  
 CC -1- PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 CC arachidonate; first step.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. ENDOPLASMIC RETICULUM  
 CC MEMBRANE AND MITOCHONDRIAL MEMBRANE.  
 CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a  
 CC peroxidase.  
 CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal anti-  
 CC inflammatory drugs such as aspirin.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.  
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DR EMBL; J03599; AAA31576.1; -  
 DR EMBL; M18243; AAA31511.1; -  
 DR EMBL; Y00750; CAA68719.1; -  
 DR PIR; A28960; A28960.  
 DR PIR; A29947; A29947.  
 DR PDB; 1PRH; 31-MAR-95.  
 DR PDB; 1PGE; 11-JAN-97.  
 DR PDB; 1PGF; 11-JAN-97.  
 DR PDB; 1PGG; 11-JAN-97.  
 DR PDB; 1PTH; 11-APR-96.  
 DR PDB; 1COE; 30-JUN-99.  
 DR PDB; 1EBV; 20-FEB-02.  
 DR PDB; 1IDY; 22-SEP-00.  
 DR PDB; 1EOG; 09-MAY-01.  
 DR PDB; 1HTS; 27-JUN-01.  
 DR PDB; 1HT8; 27-JUN-01.  
 DR PDB; 1FE2; 02-MAY-01.  
 DR PDB; 1IGX; 12-DEC-01.  
 DR PDB; 1IGZ; 12-DEC-01.  
 DR InterPro; IPR002007; Anni peroxidase.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR002016; Peroxidase.  
 DR Pfam; PF03098; An\_peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 DR Oxidoreductase; Dioxigenase; Peroxidase; Glycoprotein;  
 KM Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;  
 KW EGF-like domain; 3D-structure; Transmembrane.  
 FT SIGNAL 1 24  
 FT CHAIN 25 600 PROSTAGLANDIN G/H SYNTHASE 1.  
 FT TRANSMEM 74 82  
 FT TRANSMEM 86 92  
 FT TRANSMEM 97 105  
 FT TRANSMEM 108 122  
 FT DOMAIN 32 70  
 FT ACT\_SITE 207 207 EGF-LIKE.  
 FT ACT\_SITE 385 385 DISTAL HISTIDINE.  
 FT METAL 388 388 CYCLOOXYGENASE.  
 FT SITE 530 530 IRON (HEME AXIAL LIGAND).  
 FT DISULFID 36 47 ASPARIN-ACETYLATED SERINE.  
 FT DISULFID 41 57  
 FT DISULFID 59 69  
 FT DISULFID 37 159  
 FT CARBOHYD 569 575  
 FT CARBOHYD 68 68  
 FT CARBOHYD 144 144  
 FT CARBOHYD 410 410  
 FT VARIANT 97 97 N-LINKED (GLCNAC. . .)  
 FT VARIANT 164 164 N-LINKED (GLCNAC. . .)  
 FT VARIANT 456 456 R-LINKED (GLCNAC. . .)  
 FT VARIANT 520 520 R -> H.  
 FT VARIANT 525 525 G -> D.  
 FT VARIANT 525 525 E -> Q OR K.  
 FT MUTAGEN 385 385 M -> I.  
 FT CONFLICT 1 3 Y->F: ABOLISHES CYCLOOXYGENASE ACTIVITY.  
 FT CONFLICT 5 5 MSR -> MV (IN REF. 3).  
 FT CONFLICT 5 5 S -> G (IN REF. 2).

Query Match 62.3%; Score 2016.5; DB 1; Length 600;  
 Best Local Similarity 64.0%; Pred. No. 9.2e-150;  
 Matches 354; Conservative 92; Mismatches 106; Indels 1; Gaps 1;

QY 19 NPCCSHPCQNRGVCMVGPDOYKDCRTGTGFGNCSTPEFLFRKLFLKPTNTVHYIL 78  
 34 NPCCYFPCQHGICVAFGLDRYOCDCRRTYSGPNCITPEIWTITLRFSPSFHML 93

QY 79 THEKGFNVYNNIPIFLNAIMSVYLSRSRLIDSPPTYNADYKSNFASNLSTYTRAL 138  
 DB 94 THEKWLMDVY-NATFIRDTLRLVLTIVRSNLIPSPPTYNADHYIGMESNSVSYTRIL 152  
 QY 139 PVPDDCCPTPLGVKVKKOLPDSNEIYKLLRRKFTPDQGSMMARAFPAQHFTTHQFKT 198  
 DB 153 PSVPRDCPTPMGTGKKQLPDAEFLSRRLRRKFTPDQGTLMARFAQHFTTHQFKT 212  
 QY 199 DHKRGPAFTNGLSGVLDLNIHGETLAROKRLRFQDKMKVQIIDGEMVPTVKDTQAE 256  
 DB 213 SGKMGPGFTKALGHVDLGHITGDNLEFRQYRLPFDGKUKTOMLNGEYVPSVEAPVL 272  
 QY 259 MTPPVPEHLPAFGQEVFGLVPGIMVATITLREHNVCDVLKQEHPEWGEQFQTS 318  
 DB 273 MAYPRGIPQSQMAVGQEVFGLPGIMVATITLREHNVCDVLKQEHFTWGEQFQTA 332  
 QY 319 RLILGETIKIYEDVVOHLSGYHFKLKDEPDLLENKQOYQYONRIAEFTNTLYHMLLP 378  
 DB 333 RLILGETIKIYEEVVOQLSGYFLQKFDPELLFGAQPQYRNRIAMENQULYHMLLP 392  
 QY 379 DTFQIHDOKNYQCFIYNNISLLEHGTQFVESFTROIAGRVAGGRNVPVAVQVQASL 438  
 DB 393 DSFRVGPQDYSYEQFLFMTSMVDYGEALVDVAFSRQPRAGRGGRNIDHILVAVDVI 452  
 QY 439 DQSRQMKYQSPREYKREMLKRYESFEELTGEKMSAELEALYGDIDAVELYPALVEKP 498  
 DB 453 KESRVLRLQPFNEYKRRKGRMKRYTSFOEITGEKMAAELEELYGDIDALEFPGILLEKC 512  
 QY 499 RPDALFGEFTWEVGAFFSLKGLMGVICSPPAVMKSTGEGEFPQITNTASQSLCNV 558  
 DB 513 HNSITFGSMTEMAFPFLKGLGMPICSPPEYKASTGEGEFTVATLTKLVCIANT 572  
 QY 559 KGCEFTSFVSDP 571  
 DB 573 KTCPEVSEHVDP 585

RESULT 15  
 PGH1\_BOVIN STANDARD; PRT; 259 AA.  
 AC 062664;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Prostaglandin G/H synthase 1 (EC 1.14.99.1) (Cyclooxygenase-1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2 synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1) (Fragment).  
 DE 1) (PGH synthase 1) (PGHS-1) (PHS 1) (Fragment).  
 GN PTGS1 OR COX1 OR COX-1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE=98006431; PubMed=9348208.  
 RA Aaseelin B., Driole P., Fortier M.A.;  
 RT "Cellular mechanisms involved during oxytocin-induced prostaglandin  
 RT F2alpha production in endometrial epithelial cells in vitro: role of  
 RT cyclooxygenase-2.";  
 RL Endocrinology 138:4798-4805(1997).  
 CC -FUNCTION: May play an important role in regulating or promoting  
 CC cell proliferation in some normal and neoplastically transformed  
 CC cells (By similarity).  
 CC -CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin  
 CC H2 + A + H(2)O.  
 CC -COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per  
 CC molecule (By similarity).  
 CC -PATHWAY: Prostaglandins and thromboxanes biosynthesis from  
 CC arachidonate, first step.  
 CC -SUBUNIT: Homodimer (By similarity).  
 CC -SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane.

```

CC -1- MISCELLANEOUS: This enzyme acts both as a dioxygenase and as a
CC peroxidase.
CC -1- MISCELLANEOUS: This enzyme is the target of nonsteroidal
CC anti-inflammatory drugs such as aspirin.
CC -1- SIMILARITY: Belongs to the prostaglandin G/H synthase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF004943; AAC05591.1; -.
CC HSSP; P05979; 1EQH.
CC InterPro; IPR002007; Anim peroxidase.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR002016; Peroxidase.
CC Pfam; PF03098; An_peroxidase; 1.
CC PRINTS; PR00457; ANPEROXIDASE.
CC PROSITE; PS50292; PEROXIDASE_3; 1.
CC Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
CC Prostaglandin biosynthesis; Heme; Iron; Membrane.
CC KW
CC NON_TER 1 1
CC ACT_SITE 87 87 DISTAL HISTIDINE (BY SIMILARITY).
CC CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC NON_TER 259 259
CC SEQUENCE 259 AA; 29830 MW; 6BE0D8C343C53F9E CRC64;

Query Match 31.0%; Score 1004; DB 1; Length 259;
Best Local Similarity 70.9%; Pred. No. 3.8e-71;
Matches 183; Conservative 30; Mismatches 45; Indels 0; Gaps 0;

QY 107 SHLIDSPPTYNADYGYKSWFAFSNLSYTRALPPVDDCPTPLGYKKGKQLPDSNEIVEK 166
DB 1 SNLIPSPPTYNVAHDIDSWESFSNVSRYTRILPSVPRDCPTPMGTGKKQLPDAEFLSRR 60
QY 167 LILRRKFTIDPQGSNNMFAFPAQHTGQFFKTDHKGPAFTNGLGHGVDLNIHYGETLAR 226
DB 61 FLIRRRKFTIDPQGSNNMFAFPAQHTGQFFKTDHKGPAFTNGLGHGVDLNIHYGDNLER 120
QY 227 QRLRLRFKDGKMKYQIIDGEMYPPTVKDIOAEMITPPQVPEHLRFVAGQEVFGLVPGLM 286
DB 121 RYQLRLRFKDGKMKYQIIDGEMYPPTVKDIOAEMITPPQVPEHLRFVAGQEVFGLVPGLM 180
QY 287 YATIWLRHNRYCDVLKQEHPEWGDQLFQTSRLIIGETIKIVIEDYVOHLSGHHFKLK 346
DB 181 YATIWLRHNRYCDVLKQEHPEWGDQLFQTSRLIIGETIKIVIEDYVOHLSGHHFKLK 240
QY 347 FDEBELLFNKQFOYQRIIA 364
DB 241 FDEBELLFNKQFOYQRIIA 258

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Search completed: April 24, 2004, 07:19:43  
 Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 24, 2004, 06:19:25 ; Search time 72 Seconds

(without alignments)  
2646.847 Million cell updates/sec

Title: US-08-064-271-10

Sequence: 1 MARRALLCAVALSHSTANP.....RSGLDINPTLLKERSTEL 604

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2967	91.7	604	Q8SPQ9	Q8SPQ9 canis fami
2	2949	91.1	604	Q8SPR3	Q8SPR3 sus scrofa
3	2884	89.1	604	Q8VH41	Q8VH41 sigmodon hi
4	2862	88.4	604	Q8VH41	Q8VH41 sigmodon hi
5	2814	86.9	604	Q92SV4	Q92SV4 rattus norv
6	2606.5	80.5	561	Q92SV4	Q92SV4 rattus norv
7	2425	74.9	607	Q9PW89	Q9PW89 mus musculi
8	2417	74.7	607	Q9PW89	Q9PW89 salvelinus
9	2331	72.0	601	Q8JH43	Q8JH43 oncorhynch
10	2198	67.9	449	Q8JH43	Q8JH43 oncorhynch
11	2071.5	64.0	604	Q9TMB3	Q9TMB3 sus scrofa
12	2047	63.2	422	Q9N288	Q9N288 equus caball
13	2045.5	63.2	606	Q9N288	Q9N288 equus caball
14	2041.5	63.0	593	Q8VUQ3	Q8VUQ3 oryctolagus
15	2040.5	63.0	597	Q8VUQ3	Q8VUQ3 oryctolagus
16	2029.5	62.7	633	Q8HZR1	Q8HZR1 brachydanio
					Q8HZR1 canis fami

17	2027.5	62.6	617	Q8C1L6	Q8C1L6 mus musculu
18	2024.5	62.5	598	Q9PTN3	Q9PTN3 salvelinus
19	2013.5	62.2	624	Q9DEQ0	Q9DEQ0 oncorhynch
20	1769	54.6	339	Q81Z49	Q81Z49 homo sapien
21	1584	48.9	589	Q9GPF4	Q9GPF4 geremia fr
22	1563	48.3	330	Q8C1P1	Q8C1P1 rattus norv
23	1540.5	47.6	592	Q96J18	Q96J18 plexaura ho
24	1047	32.3	414	Q8HZR0	Q8HZR0 canis fami
25	905	28.0	178	Q9TVB3	Q9TVB3 bos taurus
26	844	26.1	164	Q8K3U5	Q8K3U5 cavia porce
27	842	26.0	178	Q7TQ43	Q7TQ43 meriones un
28	779	24.1	202	Q7TQ44	Q7TQ44 meriones un
29	734	22.7	204	Q9TMT7	Q9TMT7 sus scrofa
30	637	19.7	533	Q82V61	Q82V61 nitrosomona
31	599	18.5	128	Q9MHO0	Q9MHO0 mesocricetu
32	587	18.1	135	Q8WKE2	Q8WKE2 macropus eu
33	497	15.4	128	Q9NDG9	Q9NDG9 canis fami
34	491	15.2	99	Q9BDG9	Q9BDG9 canis fami
35	431	13.3	109	Q91ZN4	Q91ZN4 mesocricetu
36	426	13.2	80	Q9QW72	Q9QW72 mus sp. 70
37	299	9.2	92	Q9QW77	Q9QW77 oncorhynch
38	292	9.0	643	Q82031	Q82031 nicotiana t
39	289.5	8.9	99	Q9TSS6	Q9TSS6 ovis aries
40	289	8.9	643	Q9AXU5	Q9AXU5 nicotiana a
41	278	8.6	643	Q93X71	Q93X71 capsicum an
42	268.5	8.3	1432	Q18647	Q18647 caenorhabdi
43	262.5	8.1	639	Q9SGH6	Q9SGH6 arabidopsis
44	262.5	8.1	964	Q8ZMB6	Q8ZMB6 streptomyce
45	254.5	7.9	1063	Q8X1B9	Q8X1B9 uscllago ma

## ALIGNMENTS

RESULT 1  
Q8SPQ9 PRELIMINARY: FRT: 604 AA.

ID Q8SPQ9  
AC Q8SPQ9: 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Prostaglandin G/H synthase-2.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21850258; PubMed=11861541;  
RA Boutemme D., Bouchard N., Boerboom D., Jones H.E., Goff A.K.,  
RA Dore M., Stiois J.;  
RT "Molecular Characterization of Canine Prostaglandin G/H Synthase-2 and  
RT Regulation in Prostatic Adenocarcinoma Cells in Vitro."  
RL Endocrinology 143:1134-1143(2002).  
DR EMBL: AY044905; AAK97783.1; -  
DR GO: GO:0004601; F:peroxidase activity; IEA.  
DR GO: GO:0006979; P:response to oxidative stress; IEA.  
DR InterPro: IPR002007; Anm\_peroxidase.  
DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR006210; IEGF.  
DR InterPro: IPR002016; Peroxidase.  
DR Pfam: PF03098; An\_peroxidase; 1.  
DR Pfam: PF00008; EGF; 1.  
DR PRINTS: PR00457; ANPEROXIDASE.  
DR SMART: SM00181; EGF; 1.  
DR PROSITE: PS50292; PEROXIDASE\_3; 1.  
SQ SQJUNCE 604 AA; 68975 MW; 42CGFEH30DZB3928 CRC64;

Query Match 91.7%; Score 2967; DB 6; Length 604;  
Best Local Similarity 90.1%; Pred. No. 1.6e-232;  
Matches 544; Conservative 30; Mismatches 30; Indels 0; Gaps 0;  
QY 1 MARRALLCAVALSHSTANPCCSHPCQNRGVCSVGFDPYKCDCTRTGFYGENCSTPEFL 60

Db	1	MLARALVICALAAVAVRANPCSSHCQNOGICMSTGFPQYKDDCTRITGFGNCSTPEFL	60
Qy	61	TRIKLFLKPEPTNTVHYILTHFGKGVNNVNNIPFLNATMSYVLTSRSHLIDSPPTYNADY	120
Db	61	TRILVLKPEPTNTVHYILTHFGKGVNNVNNIPFLNATIMKYVLTSRSHIESPPTYNVY	120
Qy	121	GYSKWEAFNSLSYTRYALRPVYPDDCPTVLGVKKGQLPDSNETVKLLRRFIFDDPQS	180
Db	121	GYSKWEAFNSLSYTRYALRPVYPDDCPTLGMVGKKEPDSKIVAKFLRRFIFDDPQT	180
Qy	181	NMMAFFAQHETHQFECTDKHKGPAFTKGLGHGVLDLNIHYETLARQRKLRFKDGKMKY	240
Db	181	NMMAFFAQHETHQFECTDKHKGPAFTKGLGHGVLDLNIHYETLDRQKRLRFKDGKMKY	240
Qy	241	QIIGEMAPPEVCKDQAEMIYPPQVPEHLRFVAGQEVFGLVBLMMYATIMLREHNRVCD	300
Db	241	QVIDGEVVPPTVKDQVEMIRYPHPHRLGFVAGQEVFGLVBLMMYATIMLREHNRVCD	300
Qy	301	VLKQHPHWPGEQOLFQTSRLILIGETIKYIVEDYQHLSGYHFKLPDELLFNQGFQYQ	360
Db	301	VLKQHPHWPDEHRLQTSRLILIGETIKYIVEDYQHLSGYHFKLPDELLFNQGFQYQ	360
Qy	361	NRIAEENFLVHMHLLPPTQPIHOKXVYQGFIVNNSILLEGITQFVESFTRQJAGRY	420
Db	361	NRIAEENFLVHMHLLPPTQPIDOENYFQGFIVNNSILLEGITQFVESFTRQJAGRY	420
Qy	421	AGGRVNPVAVQKVSASIDQSRQMKQSYFNEYRKRFLMRYESFEELTEKEMSALEAL	480
Db	421	AGGRVNPVAVQVAVASIDQSRQMKQSYNEVRKRRLRPLPYTSFEELTEKEMVAGLEAL	480
Qy	481	YGDIDAVELYPALLVEKRPDAIFGETWYEVGAPSLKGLMGNVITSPAYWKSTGGEV	540
Db	481	YGDIDAMELYPALLVKRPDAIFGETWYEMGAPSLKGLMGNPISPYWKSTGGEV	540
Qy	541	GEQIINTASIGLIGNNVGCPETSPSVDDPELTKYVTINASSRSGLDINPTVLLKER	600
Db	541	GKRIINTASIGLIGNNVGCPETSPSVDDPELTKYVTINASSHSGLDINPTVLLKER	600
Qy	601	STEL 604	
Db	601	STEL 604	

DR	SMART: SM00181; EGF: 1.	DR	SMART: SM00181; EGF: 1.
SR	PROSITE: PSS0292; PEROXIDASE 3; 1.	SR	PROSITE: PSS0292; PEROXIDASE 3; 1.
QO	SEQUENCE 604 AA; 69145 MW; DA951E35205F9A90 CRC64;	QO	SEQUENCE 604 AA; 69145 MW; DA951E35205F9A90 CRC64;
Query Match	91.1%; Score 2949; DB 6; Length 604;	Query Match	91.1%; Score 2949; DB 6; Length 604;
Best Local Similarity	89.6%; Pred. No. 4.6e-231;	Best Local Similarity	89.6%; Pred. No. 4.6e-231;
Matches 541; Conservative 28; Mismatches 35; Indels 0; Gaps 0;		Matches 541; Conservative 28; Mismatches 35; Indels 0; Gaps 0;	
1	MLAALLLCVLAISHTANPCCHSPCCNRGCMGVDPQYKCDCTFRGFGENCSTPEFL	1	MLAALLLCVLAISHTANPCCHSPCCNRGCMGVDPQYKCDCTFRGFGENCSTPEFL
2		2	
3		3	
4		4	
5		5	
6	1 MLAAALLCAVSLCTAPKPCSNPCQNRGICMSVGDHKKCDCTFRGFGENCSTPEFL	6	1 MLAAALLCAVSLCTAPKPCSNPCQNRGICMSVGDHKKCDCTFRGFGENCSTPEFL
7		7	
8		8	
9	61 TRILFLKPEPTNTYHILLTHEKGMVNNVNNIPFLRNAIMSVLTSRSHLIDSPPTNADY	9	61 TRILFLKPEPTNTYHILLTHEKGMVNNVNNIPFLRNAIMSVLTSRSHLIDSPPTNADY
10		10	
11		11	
12	61 TRILFLKPEPTNTYHILLTHEKGMVNNVNNIPFLRNAIMSVLTSRSHLIDSPPTNADY	12	61 TRILFLKPEPTNTYHILLTHEKGMVNNVNNIPFLRNAIMSVLTSRSHLIDSPPTNADY
13		13	
14	121 GYKSWEAFSNLSYTRALPRVDDCPTPLGYKGGKQPLDSNELYKLLRKRKTPDDQGS	14	121 GYKSWEAFSNLSYTRALPRVDDCPTPLGYKGGKQPLDSNELYKLLRKRKTPDDQGS
15		15	
16	121 GYKSWEAFSNLSYTRALPRVDDCPTPLGYKGGKQPLDSNELYKLLRKRKTPDDQGS	16	121 GYKSWEAFSNLSYTRALPRVDDCPTPLGYKGGKQPLDSNELYKLLRKRKTPDDQGS
17		17	
18	181 NMMAFAFQHTHOFKPTDHRKGAFNGTGLGHVDLNIYGETLARQKRLFPDQGMKY	18	181 NMMAFAFQHTHOFKPTDHRKGAFNGTGLGHVDLNIYGETLARQKRLFPDQGMKY
19		19	
20	181 NMMAFAFQHTHOFKPTDHRKGAFNGTGLGHVDLNIYGETLARQKRLFPDQGMKY	20	181 NMMAFAFQHTHOFKPTDHRKGAFNGTGLGHVDLNIYGETLARQKRLFPDQGMKY
21		21	
22	241 QIIDGEMPTVKDQJQEMIVPQVPEHLRPAVGGEVGLVPGIMVATIMLRHNRYCD	22	241 QIIDGEMPTVKDQJQEMIVPQVPEHLRPAVGGEVGLVPGIMVATIMLRHNRYCD
23		23	
24	241 QIIDGEMPTVKDQJQEMIVPQVPEHLRPAVGGEVGLVPGIMVATIMLRHNRYCD	24	241 QIIDGEMPTVKDQJQEMIVPQVPEHLRPAVGGEVGLVPGIMVATIMLRHNRYCD
25		25	
26	301 VLKQHPHWPBGDQFLQTSRLILIGETIKIVIEDYVQHSYGHFKLKEPPELLFNQFOYO	26	301 VLKQHPHWPBGDQFLQTSRLILIGETIKIVIEDYVQHSYGHFKLKEPPELLFNQFOYO
27		27	
28	301 VLKQHPHWPBGDQFLQTSRLILIGETIKIVIEDYVQHSYGHFKLKEPPELLFNQFOYO	28	301 VLKQHPHWPBGDQFLQTSRLILIGETIKIVIEDYVQHSYGHFKLKEPPELLFNQFOYO
29		29	
30	361 NRIAEFNTLVHMHPLPDPTQIHOQKNYOOPIFNNSILLENHGTQVVESTROIAQRY	30	361 NRIAEFNTLVHMHPLPDPTQIHOQKNYOOPIFNNSILLENHGTQVVESTROIAQRY
31		31	
32	361 NRIAEFNTLVHMHPLPDPTQIHOQKNYOOPIFNNSILLENHGTQVVESTROIAQRY	32	361 NRIAEFNTLVHMHPLPDPTQIHOQKNYOOPIFNNSILLENHGTQVVESTROIAQRY
33		33	
34	421 AGGRNVPAVQVQASIDQSRQKYGQFNEFKRPFMLKPYESFEELTGKEMSALEBAL	34	421 AGGRNVPAVQVQASIDQSRQKYGQFNEFKRPFMLKPYESFEELTGKEMSALEBAL
35		35	
36	421 AGGRNVPAVQVQASIDQSRQKYGQFNEFKRPFMLKPYESFEELTGKEMSALEBAL	36	421 AGGRNVPAVQVQASIDQSRQKYGQFNEFKRPFMLKPYESFEELTGKEMSALEBAL
37		37	
38	481 YGDIDAVELYPALLVYKPPDAIFGETIYVEVAPSPSLKGMGNVICSAPYKPESTFGGEV	38	481 YGDIDAVELYPALLVYKPPDAIFGETIYVEVAPSPSLKGMGNVICSAPYKPESTFGGEV
39		39	
40	481 YGDIDAVELYPALLVYKPPDAIFGETIYVEVAPSPSLKGMGNVICSAPYKPESTFGGEV	40	481 YGDIDAVELYPALLVYKPPDAIFGETIYVEVAPSPSLKGMGNVICSAPYKPESTFGGEV
41		41	
42	541 GQIINTASTOSLGNVKGCFSTFSVDPDLITVTINASSSRSGLDIDNPVLTKER	42	541 GQIINTASTOSLGNVKGCFSTFSVDPDLITVTINASSSRSGLDIDNPVLTKER
43		43	
44	541 GQIINTASTOSLGNVKGCFSTFSVDPDLITVTINASSSRSGLDIDNPVLTKER	44	541 GQIINTASTOSLGNVKGCFSTFSVDPDLITVTINASSSRSGLDIDNPVLTKER
45		45	
46	601 STEL 604	46	601 STEL 604
47		47	
48	601 STEL 604	48	601 STEL 604
49		49	
50	601 STEL 604	50	601 STEL 604
51		51	
52	601 STEL 604	52	601 STEL 604
53		53	
54	601 STEL 604	54	601 STEL 604
55		55	
56	601 STEL 604	56	601 STEL 604
57		57	
58	601 STEL 604	58	601 STEL 604
59		59	
60	601 STEL 604	60	601 STEL 604
61		61	
62	601 STEL 604	62	601 STEL 604
63		63	
64	601 STEL 604	64	601 STEL 604
65			

DR GO: 00004601; F:peroxidase activity; IEA.  
 DR GO: 00006979; P:response to oxidative stress; IEA.  
 DR InterPro: IPR002007; AnIm\_peroxidase.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS50292; PEROXIDASE; 3; 1.  
 DR SEQUENCE 604 AA; 69084 MW; 3B4A416A5F33BAC1 CRC64;

Query Match 89.1%; Score 2884; DB 11; Length 604;  
 Best Local Similarity 87.1%; Pred. No. 8.9e-226;  
 Matches 526; Conservative 39; Mismatches 39; Indels 0; Gaps 0;

QY 1 M LARALLLCALVALSHTANPCSSHPCCNRCVMSVGFQYKCDCTRTGFGENCSTPEFL 60  
 DB 1 M LFRVAVLTCALALSHANPCSSNRCNRCGECMTVGFQYKCDCTRTGFGENCCTPEFL 60  
 QY 61 TRIKLFLKPTNTVHYILTHFKGFVNVNIPFLRNALMSYVLTSSHLIDSPTYNADY 120  
 DB 61 TRIKLFLKPTNTVHYILTHFKGFVNVNIPFLRNALMSYVLTSSHLIDSPTYNADY 120  
 QY 121 GYKSWAFSNLSYTTALPPVDDCPTPLGVKSKQLPSNNEIVEKLLRRKTIPOGGS 180  
 DB 121 GYKSWAFSNLSYTTALPPVDDCPTPLGVKSKQLPSNNEIVEKLLRRKTIPOGGS 180  
 QY 181 NMFAFAFHQFHTQFKTDHKGPAFTNGIGHGVLDNHYGETLAROKRLFKDGKMY 240  
 DB 181 NMFAFAFHQFHTQFKTDHKGPAFTNGIGHGVLDNHYGETLAROKRLFKDGKMY 240  
 QY 241 QIIDGMYPPTYKDTQAEIMTYPPQVEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300  
 DB 241 QIIDGMYPPTYKDTQAEIMTYPPQVEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300  
 QY 301 VLKQHPHMDDELQFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360  
 DB 301 VLKQHPHMDDELQFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360  
 QY 361 NRIAEFNTLYHNPPLPTFQIHQKYNQOFTYNNSSILBHGITOQVESFTROJAGRY 420  
 DB 361 NRIAEFNTLYHNPPLPTFQIHQKYNQOFTYNNSSILBHGITOQVESFTROJAGRY 420  
 QY 421 AGGRNVPVAVQKVSQSIDOSQOMKYOSFNEVYKRFMLKPYSPFEELTEKEMSALEAL 480  
 DB 421 AGGRNVPVAVQKVSQSIDOSQOMKYOSFNEVYKRFMLKPYSPFEELTEKEMSALEAL 480  
 QY 481 YGDIIDAVELYPALVLEKRPDAIFGETWVEGAPSLKGLMGVLTCSPAYMKRSTGGGV 540  
 DB 481 YGDIIDAVELYPALVLEKRPDAIFGETWVEGAPSLKGLMGVLTCSPAYMKRSTGGGV 540  
 QY 541 GFQIINTASIQSLICNNVGCPTSFVDPDELIKVTITNASSSRGLDINDPTVLKRR 600  
 DB 541 GFQIINTASIQSLICNNVGCPTSFVDPDELIKVTITNASSSRGLDINDPTVLKRR 600  
 QY 601 STEL 604  
 DB 601 STEL 604

## RESULT 4

Q63124 PRELIMINARY; PRT; 604 AA.  
 AC Q63124;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cyclooxxygenase-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE=Hippocampus;  
 RA Yamagata K.K.Y.;  
 RT "Expression of a mitogen-inducible cyclooxygenase in brain neurons:  
 RT Regulation by synaptic activity and glucocorticoids."  
 RL Neuron 0:0-0(1993).  
 DR EMBL; L20085; AAA40947.1; -.  
 DR HSSP; O05769; 1DDX.  
 DR GO: 00004601; F:peroxidase activity; IEA.  
 DR GO: 00006979; P:response to oxidative stress; IEA.  
 DR InterPro: IPR002007; AnIm\_peroxidase.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS50292; PEROXIDASE; 3; 1.  
 DR SEQUENCE 604 AA; 69130 MW; 98E7BB71080E6F0C CRC64;

Query Match 88.4%; Score 2862; DB 11; Length 604;  
 Best Local Similarity 86.3%; Pred. No. 5.5e-224;  
 Matches 521; Conservative 40; Mismatches 43; Indels 0; Gaps 0;

QY 1 M LARALLLCALVALSHTANPCSSHPCCNRCVMSVGFQYKCDCTRTGFGENCSTPEFL 60  
 DB 1 M LFRVAVLTCALALSHANPCSSNRCNRCGECMTVGFQYKCDCTRTGFGENCCTPEFL 60  
 QY 61 TRIKLFLKPTNTVHYILTHFKGFVNVNIPFLRNALMSYVLTSSHLIDSPTYNADY 120  
 DB 61 TRIKLFLKPTNTVHYILTHFKGFVNVNIPFLRNALMSYVLTSSHLIDSPTYNADY 120  
 QY 121 GYKSWAFSNLSYTTALPPVDDCPTPLGVKSKQLPSNNEIVEKLLRRKTIPOGGS 180  
 DB 121 GYKSWAFSNLSYTTALPPVDDCPTPLGVKSKQLPSNNEIVEKLLRRKTIPOGGS 180  
 QY 181 NMFAFAFHQFHTQFKTDHKGPAFTNGIGHGVLDNHYGETLAROKRLFKDGKMY 240  
 DB 181 NMFAFAFHQFHTQFKTDHKGPAFTNGIGHGVLDNHYGETLAROKRLFKDGKMY 240  
 QY 241 QIIDGMYPPTYKDTQAEIMTYPPQVEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300  
 DB 241 QIIDGMYPPTYKDTQAEIMTYPPQVEHLRFVAGQEVFGVPGIMMYATITWREHNRVCD 300  
 QY 301 VLKQHPHMDDELQFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360  
 DB 301 VLKQHPHMDDELQFQTSRLILGETIKIVIEDYVQHLSGYHFKLKFDELLFNQOFQY 360  
 QY 361 NRIAEFNTLYHNPPLPTFQIHQKYNQOFTYNNSSILBHGITOQVESFTROJAGRY 420  
 DB 361 NRIAEFNTLYHNPPLPTFQIHQKYNQOFTYNNSSILBHGITOQVESFTROJAGRY 420  
 QY 421 AGGRNVPVAVQKVSQSIDOSQOMKYOSFNEVYKRFMLKPYSPFEELTEKEMSALEAL 480  
 DB 421 AGGRNVPVAVQKVSQSIDOSQOMKYOSFNEVYKRFMLKPYSPFEELTEKEMSALEAL 480  
 QY 481 YGDIIDAVELYPALVLEKRPDAIFGETWVEGAPSLKGLMGVLTCSPAYMKRSTGGGV 540  
 DB 481 YGDIIDAVELYPALVLEKRPDAIFGETWVEGAPSLKGLMGVLTCSPAYMKRSTGGGV 540  
 QY 541 GFQIINTASIQSLICNNVGCPTSFVDPDELIKVTITNASSSRGLDINDPTVLKRR 600  
 DB 541 GFQIINTASIQSLICNNVGCPTSFVDPDELIKVTITNASSSRGLDINDPTVLKRR 600  
 QY 601 STEL 604  
 DB 601 STEL 604

## RESULT 5

Q925V4 PRELIMINARY; PRT; 604 AA.  
 AC Q925V4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBrel. 19, last sequence update)  
 DT 01-OCT-2003 (TReMBrel. 25, last annotation update)  
 DE Cyclooxygenase-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20390055; PubMed=10816563;  
 RA Xu K., Robida A.M., Murphy T.J.;  
 RT "Immediate-early MEK-1-dependent Stabilization of Rat Smooth Muscle  
 Cell Cyclooxygenase-2 mRNA by G-protein-coupled Receptor Signaling.";  
 RL J Biol. Chem. 275:23012-23019(2000).  
 DR EMBL: AF233596; AAF36986.1; -  
 DR GO: GO:0004601; Peroxidase activity; IEA.  
 DR GO: GO:0006979; Response to oxidative stress; IEA.  
 DR InterPro: IPR002007; Anion peroxidase.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An. peroxidase; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR PROSITE: PS50292; PEROXIDASE\_3; 1.  
 SQ SEQUENCE 604 AA; 69234 MW; 3FBD4E73FF4965F CRC64;  
 Query Match 86.9%; Score 2814; DB 11; Length 604;  
 Best Local Similarity 84.9%; Pred. No. 4.4e-220;  
 Matches 513; Conservative 41; Mismatches 50; Indels 0; Gaps 0;

QY 1 MLRAALLICAVALLSHTANPCSHPCNRCVMSVGFQYKCDCTRTGFYGENCSTPEFL 60  
 Db 1 MLRAVAVLLCAGPGLSHANPCSCNRCGECMSIGDQYKCDCTRTGFYGENCSTPEFL 60  
 QY 61 TRIKLPKPTPNVTHYLTHFKGFWNVNNIPRLRNAINSVLTSTRSHLIDSEPTVADY 120  
 Db 61 TRIKLPKPTPNVTHYLTHFKGFWNVNNIPRLRIQSMRYVLTSTRSHLIDSEPTVADY 120  
 QY 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSNEIYEKLLRRKFPDPQGS 180  
 Db 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSKEVLEKYLRRREFPDQST 180  
 QY 181 NMWFAFPAQHTHQEFKTDHKGPAFTNGLGHVLDNHYGETLARQKRLFPDGMKY 240  
 Db 181 NMWFAFPAQHTHQEFKTDHKGPAFTNGLGHVLDNHYGETLDRGHKRLFPDGLKXY 240  
 QY 241 QIIDGEMVPTVADTQEMTYPPOVPHLRPAVQEVGLVPGIMATYTLRHHNVCD 300  
 Db 241 QVIGGEVYPTVADTQEMTYPPIPHLRPAVQEVGLVPGIMATYTLRHHNVCD 300  
 QY 301 VLKQEHFEMGDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFQY 360  
 Db 301 ILKQEHFEMGDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFQY 360  
 QY 361 NRIAEFNTLYHMHPLLPTFQIHDKQKYNQOFTYNNSSILLEGITQVASFTRQAGRY 420  
 Db 361 NRIAEFNTLYHMHPLLPTFQIHDKQKYNQOFTYNNSSILLEGITQVASFTRQAGRY 420  
 QY 421 AGGNVPAVQKYSQASIDSRQKQYSPFHYRRKRLKPESEELTGEKMAELAL 480  
 Db 421 AGGNVPAVQKYSQASIDSRQKQYSPFHYRRKRLKPESEELTGEKMAELAL 480  
 QY 481 YGIDAVELVYVALLVERPRDAIFGETMVEVGAFFSLKGLMGNVICSPAYWKPSTFGGEV 540  
 Db 481 YHIDDAVELVYVALLVERPRDAIFGETMVEVGAFFSLKGLMGNVICSPOYKWPSTFGGEV 540  
 QY 541 GFRIINTASIQSLICNNVKGCPFTSFVDPBELIKVTYINASSRSGLDINPTVLKER 600  
 Db 541 GFRIINTASIQSLICNNVKGCPFTSFVDPBELIKVTYINASSRSGLDINPTVLKER 600  
 QY 601 STEL 604  
 Db 601 STEL 604

RESULT 6  
 Q7TW2 PRELIMINARY; PRT; 561 AA.  
 ID Q7TW2;  
 AC Q7TW2;  
 DT 01-OCT-2003 (TReMBrel. 25, Created)  
 DT 01-OCT-2003 (TReMBrel. 25, last sequence update)  
 DT 01-OCT-2003 (TReMBrel. 25, last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC052900; AAH52900.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 561 AA; 63857 MW; 1CC5F645AD6738B5 CRC64;  
 Query Match 80.5%; Score 2606.5; DB 11; Length 561;  
 Best Local Similarity 79.5%; Pred. No. 3e-203;  
 Matches 480; Conservative 39; Mismatches 42; Indels 43; Gaps 1;

QY 1 MLRAALLICAVALLSHTANPCSHPCNRCVMSVGFQYKCDCTRTGFYGENCSTPEFL 60  
 Db 1 MLRAVAVLLCAGPGLSHANPCSCNRCGECMSIGDQYKCDCTRTGFYGENCSTPEFL 60  
 QY 61 TRIKLPKPTPNVTHYLTHFKGFWNVNNIPRLRNAINSVLTSTRSHLIDSEPTVADY 120  
 Db 61 TRIKLPKPTPNVTHYLTHFKGFWNVNNIPRLRSILMKYVLTSTRSHLIDSEPTVADY 120  
 QY 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSNEIYEKLLRRKFPDPQGS 180  
 Db 121 GYSWMEFSLSYSTRALPEVPDDCPTPLGVKGGKOLPDSKEVLEKYLRRREFPDQGS 180  
 QY 181 NMWFAFPAQHTHQEFKTDHKGPAFTNGLGHVLDNHYGETLARQKRLFPDGMKY 240  
 Db 181 NMWFAFPAQHTHQEFKTDHKGPAFTNGLGHVLDNHYGETLDRGHKRLFPDGLKXY 240  
 QY 241 QIIDGEMVPTVADTQEMTYPPOVPHLRPAVQEVGLVPGIMATYTLRHHNVCD 300  
 Db 241 QVIGGEVYPTVADTQEMTYPPIPHLRPAVQEVGLVPGIMATYTLRHHNVCD 300  
 QY 301 VLKQEHFEMGDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFQY 360  
 Db 301 VLKQEHFEMGDEQLFQTSRLILIGETIKIYIEDVYVGHLSGHNFLKRPDELLFNKQFQY 360

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QY 361 NR1AEFNTLYHMHPLPDTFQIHDOXKYNQOFTYNNLSLLEHGTQVSEFTQIAGR 420
Db 318 NR1ASENTLYHMHPLPDTFQIHDOXKYNQOFTYNNLSLLEHGTQVSEFTQIAGR 377
QY 421 AGGNVPPAVOKVSOASIDSRQMKYOSFNEYRFRFMKPESEFEELTGKEMSAELAL 480
Db 378 AGGNVPLAVQAVAKASIDSRQMKYOSFNEYRFRFMKPESEFEELTGKEMSAELAL 437
QY 481 YGDIIDAVELYPALLVEKRPDAIFGETMVEGAPFSLKGLMGVNICSPAYWKPESTFGGEV 540
Db 438 YSIDIVVELYPALLVEKRPDAIFGETMVEGAPFSLKGLMGVNICSPAYWKPESTFGGEV 497
QY 541 GFOIINTASIOSLICNNVKGCPTFSVPDPPELTKYTTINASSRSGLDINDPTVLKER 600
Db 498 GFKINTASIOSLICNNVKGCPTFSVPDPPELTKYTTINASSRSGLDINDPTVLKER 557
QY 601 STEL 604
Db 558 STEL 561

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## RESULT 7

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Q9PM89 PRELIMINARY; PRT; 607 AA.
ID Q9PM89
AC Q9PM89;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Prostaglandin endoperoxide synthase-2.
GN PGS-2.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCB1_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=20181763; PubMed=10715542;
RA Roberts S.B., Langenau D.M., Goetz F.W.;
RT "Cloning and characterization of prostaglandin endoperoxide synthase-1
RT and -2 from the brook trout update."
RL Mol. Cell. Endocrinol. 160:89-97(2000).
DR EMBL: AF158373; AAD45896.1; -.
DR HSSP: 005769; ICYU.
DR GO: GO:0004601; F:peroxidase activity; IEA.
DR GO: GO:0006979; P:response to oxidative stress; IEA.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF003098; An_peroxidase; 1.
DR Pfam: PF00008; EGF; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
SQ SEQUENCE 607 AA; 69150 MW; 91CBF27BAEDD96B0 CRC64;

```

Query Match 74.9%; Score 2425; DB 13; Length 607;  
 Best Local Similarity 71.7%; Pred. No. 188;  
 Matches 431; Conservative 81; Mismatches 85; Indels 4; Gaps 3;

```

QY 6 LLLCAVLASHTANPCGSHPCONRGVMSVGFDOYKCCCTTGTFGENGCTPEFLTKL 65
Db 9 LLLVGLYFCGCVDPCCACQPCENRGLCNKSGFVDECCCTTGYYGKNCCTPEFLTWIKI 68
QY 66 FLKPTPTVHYLTHFKGFNVVANNIPFLRNAIMSYYLTSSHLIDSPPTNADYGYKSW 125
Db 69 SLKDPMTVHYLTHYGLMWVINKITFVRNAIMSYYLTSSHLIDSPPTNADYGYKSW 128
QY 126 EAFENLSYTRALPPVDDCTPELVGYGKKQLPSNSETVEKLLLRKRTDPDQGSNMFA 185
Db 129 EAYNLSYTRALPPVDDCTPELVGYGKKQLPSNSETVEKLLLRKRTDPDQGSNMFA 188
QY 186 FFAQHTHOFKTDHKKGPATNGLGSHVDLNIHYGELTAQRKLRFKQGMKTYQIIDD 245

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Db 189 FFAQHTHOFKTDHKKGPATNGLGSHVDLNIHYGELTAQRKLRFKQGMKTYQIIDD 248
QY 246 EMTPEPTVKTQAMTIPPQVBEHLRPAVGOEVLVGLMMVATITWIREHNRVCDVYKOE 305
Db 249 EMTPEPTVKTQAMTIPPQVBEHLRPAVGOEVLVGLMMVATITWIREHNRVCDVYKOE 308
QY 306 HPEMGEQLFQTRILLIGTTIKIVIEDVYQHLGSHFKLKEPDELLFNKQFOYONIAA 365
Db 309 HPEMGEQLFQTRILLIGTTIKIVIEDVYQHLGSHFKLKEPDELLFNKQFOYONIAA 368
QY 366 EFTLYHMHPLPDTFQIHDOXKYNQOFTYNNLSLLEHGTQVSEFTQIAGR 425
Db 369 EFTLYHMHPLPDTFQIHDOXKYNQOFTYNNLSLLEHGTQVSEFTQIAGR 428
QY 426 VPPAVOKVSOASIDSRQMKYOSFNEYRFRFMKPESEFEELTGKEMSAELAL 485
Db 429 VPPAVOKVSOASIDSRQMKYOSFNEYRFRFMKPESEFEELTGKEMSAELAL 488
QY 486 AVELYPALLVEKRPDAIFGETMVEGAPFSLKGLMGVNICSPAYWKPESTFGGEV 545
Db 489 AVELYPALLVEKRPDAIFGETMVEGAPFSLKGLMGVNICSPAYWKPESTFGGEV 548
QY 546 NTASIOSLICNNVKGCPTFSVPDPPELTKYTTINASSRSGLDINDPTVLKER 603
Db 549 NTASIOSLICNNVKGCPTFSVPDPPELTKYTTINASSRSGLDINDPTVLKER 606
QY 604 L 604
Db 607 L 607

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## RESULT 8

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Q9W715 PRELIMINARY; PRT; 607 AA.
ID Q9W715
AC Q9W715;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cyclooxygenase-2 precursor.
GN COX-2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCB1_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Zou J., Neuman N., Holland J., Belosevic M., Cunningham C.,
RA "Fish macrophages express a cyclooxygenase-2 homologue following
RT activation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ238307; CAB46017.1; -.
DR HSSP: 005769; ICYU.
DR GO: GO:0004601; F:peroxidase activity; IEA.
DR GO: GO:0006979; P:response to oxidative stress; IEA.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF003098; An_peroxidase; 1.
DR Pfam: PF00008; EGF; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
SQ SEQUENCE 607 AA; 69384 MW; 6EFA43C04CD3D9 CRC64;

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Query Match 74.7%; Score 2417; DB 13; Length 607;  
 Best Local Similarity 71.2%; Pred. No. 88-188;  
 Matches 428; Conservative 82; Mismatches 87; Indels 4; Gaps 3;

QY 6 LLLCAVALSHSHTANCCSHPCONRGVMSVGFQYKCDCTRTGFGYNGSTPELITRL 65  
 DB 9 LLLAAGLVFCEGVDCCAQPCENRGICNSKGFNDCCCTRTGYYGKNCCTPELITWIKI 68  
 QY 66 FLKPEPNTVHYILTHFKGFNNVNNIPLRNAIMSIVLTSRSHLIDSPPTVADYGYSW 125  
 DB 69 SIKPEPNTIHYILTHYKGLMNVINKITFRNAIMSIVLTPRSHLVDSPTVADYGYSW 128  
 QY 126 EAFSNLSYVTRALPVPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIIDPQSSNMFA 185  
 DB 129 EAYSNLFYTRTLPLPLPKCCPTPMGTAGRAVLPDVKLVEKVLIRKRFIDPQSSNMFA 188  
 QY 186 PFAQHFTHQFETKDHKGPAFTNGLGHVLDLNIHYGETLARQRKLRPFQDMGKKQIIDG 245  
 DB 189 PFAQHFTHQFETKDHKGPAFTNGLGHVLDLNIHYGETLARQRKLRPFQDMGKKQIIDG 248  
 QY 246 EYRPTVAKDTQAEMLTYPPOVPEHLRFVAVGQEVFGVGLPMYATITLREHNRVCVLCOE 305  
 DB 249 EYRPTVAVGQAEMLTYPPOVPEHLRFVAVGQEVFGVGLPMYATITLREHNRVCVLCOE 308  
 QY 306 HPEWGEQDLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFYQNR1A 365  
 DB 309 HPEWDERIFQTTRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFYQNR1A 368  
 QY 366 EENTLYHMHPLPDTFQIHDOKNYQOFTYNNLSILHEG1QFVESFTROIAGRVAGRN 425  
 DB 369 EENTLYHMHPLPDTFQIHDOKNYQOFTYNNLSILHEG1QFVESFTROIAGRVAGRN 428  
 QY 426 VPPAVQVQASIDQSRQMKYQSFNEYRKRFLKPYSEFEELTGKEMSAELBALYGDID 485  
 DB 429 LPPALVGAAKLLEHSDRQYQSLNAYRRFPMRYTSFEDLTGETLAELESTIYGDVD 488  
 QY 486 AVELYPALIVEKRPDAITFGETWVEGAPPSLKGMLGNVITCSPAYKKESTFGGEVFOII 545  
 DB 489 AVELYGLIVERPRAVGEETWVEGAPPSLKGMLGNVITCSPAYKKESTFGGEVFOII 548  
 QY 546 NTAISIOSLICNNVKG-CPTFSVDPD-PELITVITINASSRSGLDINPTVYLKKESTE 603  
 DB 549 NTAISLRLICNNVKGSCPMVSFOVDFPLRAFESASVNTSEAH-LSDMNFQVILKERTSE 606  
 QY 604 L 604  
 DB 607 L 607

RESULT 9  
 Q8UH43 PRELIMINARY; PRT; 601 AA.  
 ID 08UH43  
 AC 08UH43  
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Prostaglandin G/H synthase 2.  
 GN PTGS2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCB1\_TaxID=7955;  
 RN NCB1\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12011329;  
 RA Grosser T., Yustiff S., Cheskis E., Pack M.A., Fitzgerald G.A.;  
 RT "Developmental expression of functional cyclooxygenases in  
 RT zebrafish."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:8418-8423 (2002).  
 DR EMBL: AY028585; AAK3031.1; -.  
 DR GO: GO:0004601; F:peroxidase activity; IEA.  
 DR GO: GO:0006979; P:response to oxidative stress; IEA.  
 DR InterPro: IPR002007; Antim\_peroxidase.  
 DR InterPro: IPR006209; BGF like.  
 DR InterPro: IPR002016; Peroxidase.

DR Pfam; PF03098; An\_peroxidase; 1.  
 DR Pfam; PF00008; BGF; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR PROSITE: PS02922; PEROXIDASE\_3; 1.  
 SQ SEQUENCE 601 AA; 68672 MW; A3852C56521DD0C1 CRC64;  
 Query Match 72.0%; Score 2331; DB 13; Length 601;  
 Best Local Similarity 67.8%; Pred. No. 8,6e-181;  
 Matches 410; Conservative 95; Mismatches 86; Indels 14; Gaps 3;  
 QY 7 LLLCAVALS-----HTANPCSCSHPCONRGVMSVGFQYKCDCTRTGFGYNGSTPELITRL 60  
 DB 4 LVCIVLSSIMWIFPEBGVDPCCAQPCQNGVCLSGADAYBCDCTRTGFGYNGCTPELITRL 63  
 QY 61 TRIKLEKPTNTVHYILTHFKGFNNVNNIPLRNAIMSIVLTSRSHLIDSPPTVADY 120  
 DB 64 TRIKALKPRNVVHYILTHYKGLMNVINKITFRNAIMSIVLTPRSHLVDSPTVADYGYSW 123  
 QY 121 GYKSWAENSLSYVTRALPVPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIIDPQGS 180  
 DB 124 GYKSWAENSLSYVTRALPVPVDDCPTPLGVKGGKQLPDSNEIVEKLLRRKFIIDPQGS 176  
 QY 181 NMFAFPFAQHFTHQFETKDHKGPAFTNGLGHVLDLNIHYGETLARQRKLRPFQDMGKKY 240  
 DB 177 SLMFAPFAQHFTHQFETKDHKGPAFTNGLGHVLDLNIHYGETLARQRKLRPFQDMGKKY 236  
 QY 241 QIIDEMVPTVKDTQAEMLTYPPOVPEHLRFVAVGQEVFGVGLPMYATITLREHNRVCD 300  
 DB 237 QVVDDEVVPLVAKDVQVEHNYPHIPEQKFAVGHAFGLVGLPMYATITLREHNRVCD 296  
 QY 301 VIKQHPHWDQDLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFYQ 360  
 DB 297 IKQHPHWDQDLFQTSRLILIGETIKIVIEDYVQHLSGYHFKLKPDELLFNKQFYQ 356  
 QY 361 NTAISLRLICNNVKG-CPTFSVDPD-PELITVITINASSRSGLDINPTVYLKKESTE 420  
 DB 357 NTAISLRLICNNVKGSCPMVSFOVDFPLRAFESASVNTSEAH-LSDMNFQVILKERTSE 416  
 QY 421 AGRNVPVAVQVQASIDQSRQMKYQSFNEYRKRFLKPYSEFEELTGKEMSAELBALY 480  
 DB 417 SGRNVPVAVQVQASIDQSRQMKYQSFNEYRKRFLKPYSEFEELTGKEMSAELBALY 476  
 QY 481 YGDIIDAVELYPALIVEKRPDAITFGETWVEGAPPSLKGMLGNVITCSPAYKKESTFG 540  
 DB 477 YGDIIDAVELYPALIVEKRPDAITFGETWVEGAPPSLKGMLGNVITCSPAYKKESTFG 536  
 QY 541 GQIINTASIOSLICNNVKG-CPTFSVDPD-PELITVITINASSRSGLDINPTVYLKKE 599  
 DB 537 GQIINTASIOSLICNNVKGSCPMVSFOVDFPLRAFESASVNTSEAH-LSDMNFQVILKERTSE 596  
 QY 600 RSTEL 604  
 DB 597 RSTEL 601

RESULT 10  
 Q9TT26 PRELIMINARY; PRT; 449 AA.  
 ID 09TT26  
 AC 09TT26  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Cyclooxygenase-2 (Fragment).  
 GN COX-2.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OC NCB1\_TaxID=9823;  
 RN NCB1\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=bred yorkshire-landrace; TISSUE=Endometrium;  
 RA Palin M.F., Guay F., Beaudry D., Laforest J.P., Matte J.J.;  
 RT "Expression of cyclooxygenase-1 (COX-1) and cyclooxygenase-2 (COX-2)



RT in swine endometrial tissue."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF207824; AAF20942.1; -.  
 DR HSPB; Q05769; IDXX.  
 DR GO: GO:0004601; F:peroxidase activity; IEA.  
 DR GO: GO:0006979; P:response to oxidative stress; IEA.  
 DR InterPro: IPR002007; Anim\_peroxidase.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 FT NON TER 1  
 FT NON TER 449  
 SQ SEQUENCE 449 AA; 52268 MW; 5910B7CC2A7CA17F CRC64;

Query Match 67.9%; Score 2198; DB 6; Length 449;  
 Best Local Similarity 90.0%; Pred. No. 3,7e-170;  
 Matches 404; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

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QY 88 VNNIPPLRNALMSYVTSRSHLIDSPPTNADYGYKSWAENSLSYTRALPEVPDDCPT 147
Db 1 VNNIPPLRNALMSYVTSRSHLIDSPPTNADYGYKSWAENSLSYTRALPEVPDDCPT 60
QY 148 PLGVKSKQLPDSNEIVEKLLLRKFTPPQSGSNMMAFEAOFHTQFRTDHRKGPART 207
Db 61 PMGVKSKRLPDSKEVEKLLLRKFTPPQSGSNMMAFEAOFHTQFRTDHRKGPART 120
QY 208 NGLGHGVNDLNTYGETFLARQKRLRFKDKRMKQIIDGEMYPPTVDOAEMTYPQVE 267
Db 121 KQCGHGVNDLSHYGESLFRQHKRLRFKDKRMKQIIDGEMYPPTVDOAEMTYPQVE 180
QY 268 HLRFAVGVGVGLVRLMMYATITLREHNRVCDVLKQEHPEWDEQLFQTSRLILGETI 327
Db 181 HLRFAVGVGVGLVRLMMYATITLREHNRVCDVLKQEHPEWDEQLFQTSRLILGETI 240
QY 328 KIVIEDYVOHLGSHYFKLKFDELLFNKQFOYONRIAENLTMHMLLPTPTQIHOK 387
Db 241 KIVIEDYVOHLGSHYFKLKFDELLFNKQFOYONRIAENLTMHMLLPTPTQIHOK 300
QY 388 YNYQOPIYNNLILHGGITQFVESFTROIAGRVAGGRNVPRAVKVQSASIDOSROMKY 447
Db 301 YNYQOPIYNNLILHGGITQFVESFTROIAGRVAGGRNVPRAVKVQSASIDOSROMKY 360
QY 448 SNEKRRKPMKPYSPFELTGEKMSALELALYGDIDAVELYPALLVEKPPDAIFGFT 507
Db 361 SNEKRRKPMKPYSPFELTGEKMSALELALYGDIDAVELYPALLVEKPPDAIFGFT 420
QY 508 MVEVGAPFSIKGLMGNVICSPAYWKSTF 536
Db 421 MVEVGAPFSIKGLMGNVICSPAYWKSTF 449

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## RESULT 11

Q7TFB3 PRELIMINARY; PRT; 604 AA.  
 AC Q7TFB3;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Rh10.  
 OS Rhesus cytomegalovirus (strain 68-1) (RHCMV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 CX NCBI\_TaxID=103930;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=68-1;  
 RX PubMed=12767982;  
 RA Hansen S.G., Strelow L.I., Franchi D.C., Anders D.G., Wong S.W.;  
 RT "Complete Sequence and Genomic Analysis of Rhesus Cytomegalovirus";  
 RL J. Virol. 77:6620-6636(2003).  
 DR EMBL: AY186194; AAF50751.1; -.  
 SQ SEQUENCE 604 AA; 68380 MW; 6699FED8F7D44D5 CRC64;

Query Match 64.0%; Score 2071.5; DB 12; Length 604;  
 Best Local Similarity 63.4%; Pred. No. 1.1e-159;  
 Matches 330; Conservative 73; Mismatches 119; Indels 33; Gaps 6;

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QY 6 LILCAVIALSHNTAPCCSHPCQNRGVGMSGFQYQCDCTRGTGEBNCSPEFLRIKL 65
Db 7 VLIVSYLSHSRQPLILPSVSRKICMTYGFHHYKDCDCHTGHFDHCTT---TRIKL 62
QY 66 FLKPTNTYHYIITHKGFNNVNNIPLRNALMSYVTSRSHLIDSPPTNADYGYKSW 125
Db 63 FLKPDPTVYTLTHFSTITWLVNNIPLRNALMSYVTSRSHLIDSPPTNADYGYKSW 122
QY 126 EAFSNLSYTRALPEVPDDCPTPLGVK-GRKQLPDSNEIVEKLLLRKFTPPQSGSNMF 184
Db 123 EAFSNLSYTRALPEVPDDCPTPLGVKGRKQLPDAHAHVEKLLLRRTFTPPQSGTNLMF 182
QY 185 AFEAOFHTQFRTDHRKGPARTNGLGHGVNDLNTYGETFLARQKRLRFKDKRMKQIID 244
Db 183 AFEAOFHTQFRTDHRKGPARTNGLGHGVNDLNTYGETFLARQKRLRFKDKRMKQIID 242
QY 245 GEMYPPTVDOAEMTYPQVEHLRFVAGQEVFGLVPGIMYATITLREHNRVCDVLKQ 304
Db 243 GEMYPPTVDOAEMTYPQVEHLRFVAGQEVFGLVPGIMYATITLREHNRVCDVLKQ 302
QY 305 EHPEDWDEQLFQTSRLILGETIKIVIEDYVOHLGSHYFKLKFDELLFNKQFOYONRIA 364
Db 303 EHPEDWDEQLFQTSRLILGETIKIVIEDYVOHLGSHYFKLKFDELLFNKQFOYONRIA 362
QY 365 AEFNTLTMHMLLPTPTQIHOKYNYQOPIYNNLILHGGITQFVESFTROIAGRVAGGR 424
Db 363 SEFNLMYHMSLMPAFELDKTYDINLVNNSILMTHGITQLYBSFTKQIAGRVAPL 422
QY 425 NVPRAVKVQSASIDOSROMKYSPNEYRKRMKPYE-SPELITGEKMSALELALYGD 483
Db 423 NL--SIIVHVVFTVMQNV-----LIMCPMHFIFINTGEEKIAELALYGD 469
QY 484 IDAVELYPALLVEKPPDAIFGFTMVEVGAPFSIKGLMGNVICSPAYWKSTFGGEVGFQ 543
Db 470 IEAVELYPALLVEKPPDAIFGFTMVEVGAPFSIKGLMGNVICSPAYWKSTFGGEVGFQ 529
QY 544 IINTASIOSLICNNYKGPFTSFVSVDPELAK-----TYTINASSRSRGID 589
Db 530 IVKSATIGSIVCSNVKGPFLAFAFRPNKELLKARNGSSSSSPSPSSSSSPSVQ 589
QY 590 DINPVLAKERSTEL 604
Db 590 HVDPEGVTKREHAEI 604

```

## RESULT 12

Q9N288 PRELIMINARY; PRT; 422 AA.  
 AC Q9N288;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Cyclooxygenase-2 (Fragment).  
 GN COX-2.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 CX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Thoroughbred; TISSUE=Arterial endothelium;  
 RA Ishida N., Sato F., Hasegawa T.;  
 RT "Molecular cloning of equine COX-2 mRNA for cyclooxygenase-2";  
 RL submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB041771; BA094762.1; -.  
 DR HSPB; Q05769; IDXX.  
 DR GO: GO:0004601; F:peroxidase activity; IEA.  
 DR GO: GO:0006979; P:response to oxidative stress; IEA.

DR InterPro; IPR002007; Anim. peroxidase.  
 DR InterPro; IPR002016; Peroxidase.  
 DR Pfam; PF03098; An. peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 FT NON TER 1 422 1  
 FT SEQUENCE 422 AA; 48675 MW; 8F9792D936BCTB63 CRC64;  
 SQ  
 Query Match 63.2%; Score 2047; DB 6; Length 422;  
 Best Local Similarity 89.6%; Pred. No. 6.5e-158;  
 Matches 378; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

QY 131 LSYTRALPPVDDCPPLGVGKQQLPDSNIVEKLLRKEIPDQSNMFAFAFH 190  
 DB 1 LSYTRALPPVADGCPPLGVGKQQLPDSNIVEKLLRKEIPDQSNMFAFAFH 60  
 QY 199 PTHQFETDHRKPAFTNGLGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYP 250  
 DB 61 PTHQFETDHRKPAFTNGLGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYP 120  
 QY 251 TVKDTQAEIYPPQVEHLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPKMG 310  
 DB 121 TVKDTQAEIYPPQVEHLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPKMG 180  
 QY 311 DQQLPQTSKLLIGETIKIVIEDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTL 370  
 DB 181 DQQLPQTSKLLIGETIKIVIEDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTL 240  
 QY 371 YHMHPLPPTFOIHDQKYNVQFIYNNISILBHGITQVESFTRQAGRVAGGRVPPAV 430  
 DB 241 YHMHPLPPTFOIHDQKYNVQFIYNNISILBHGITQVESFTRQAGRVAGGRVPPAV 300  
 QY 431 QKVSQASIDQSRQKYSFNEHYKRFMLKPYESFEELTGKEMSALEALYGDIDAVEIY 490  
 DB 301 QKVSQASIDQSRQKYSFNEHYKRFMLKPYESFEELTGKEMSALEALYGDIDAVEIY 360  
 QY 491 PALVKKRPDPAIFGFTWVEVGFSLKGLMGVIVICSPAYWKSTGEGEVGOIINTASI 550  
 DB 361 PALVKKRPDPAIFGFTWVEVGFSLKGLMGVIVICSPAYWKSTGEGEVGOIINTASI 420  
 QY 551 QS 552  
 DB 421 QS 422

RESULT 13  
 ID 097554 PRELIMINARY; PRT; 606 AA.  
 AC 097554;  
 DT 01-MAY-1999 (TEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Cyclooxygenase-1.  
 GN COX-1.  
 OS Oryzctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryzctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand White;  
 RA Guan Y., Zhang Y., Breyer R.M., Davis L., Redha R., Chang S.,  
 RT "Intrarenal localization of cyclooxygenase-1 and -2 and their  
 RT differential expression in acute hydropnephrotic kidney";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF026008; AAD01796.1; -  
 DR HSSP; P05979; 1COE  
 DR GO; GO:0004601; P:peroxidase activity; IEA.  
 DR GO; GO:0006979; P:response to oxidative stress; IEA.  
 DR InterPro; IPR002007; Anim. peroxidase.  
 DR InterPro; IPR006210; IEGF.

DR InterPro; IPR002016; Peroxidase.  
 DR Pfam; PF03098; An. peroxidase; 1.  
 DR PRINTS; PR00457; ANPEROXIDASE.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
 SQ SEQUENCE 606 AA; 69075 MW; DB751FD1E2FICD77 CRC64;  
 Query Match 63.2%; Score 2045.5; DB 6; Length 606;  
 Best Local Similarity 85.1%; Pred. No. 1.5e-157;  
 Matches 370; Conservative 85; Mismatches 112; Indels 19; Gaps 4;

QY 19 NPCCSHPCQNRGVCMSVGFQYKDCDCTRTGYGNCSTPEELTRIKLPLKPTPTVHIL 78  
 DB 40 NPCCSHPCQNRGVCMSVGFQYKDCDCTRTGYGNCSTPEELTRIKLPLKPTPTVHIL 99  
 QY 79 THKGFNVNVPNIPPLNANMSYVLTSHSLIDSPPTNADVGYSWEAFNSLXYTRAL 138  
 DB 100 THKGFNVNVPNIPPLNANMSYVLTSHSLIDSPPTNADVGYSWEAFNSLXYTRAL 158  
 QY 139 PVPDDCPTPLGVKQKQQLPDSNIVEKLLRKEIPDQSNMFAFAFHHTQFET 198  
 DB 159 PVPDDCPTPLGVKQKQQLPDSNIVEKLLRKEIPDQSNMFAFAFHHTQFET 218  
 QY 199 DHRGPATNGIGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYPPTVADQAE 258  
 DB 219 DHRGPATNGIGHVDLNIHYGETLARQRLRFKQKMYQIIDGEMYPPTVADQAE 278  
 QY 259 MLYPPQVEHLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPKMG 318  
 DB 279 MLYPPQVEHLRFVAGQVEFGLVPGMMYATITWREHNRVCDVTKQHPKMG 338  
 QY 319 RLILIGETIKIVIEDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTLYHMHPLP 378  
 DB 339 RLILIGETIKIVIEDYVQHLSGYHFKLKEDELLFNKQFOYONRIAEFNTLYHMHPLP 398  
 QY 379 DFPQHDQKYNVQFIYNNISILBHGITQVESFTRQAGRVAGGRVPPAVQKVSQASI 438  
 DB 399 DFPQHDQKYNVQFIYNNISILBHGITQVESFTRQAGRVAGGRVPPAVQKVSQASI 458  
 QY 439 DQSRQKYSFNEHYKRFMLKPYESFEELTGKEMSALEALYGDIDAVEIYPALVKKRP 498  
 DB 459 DQSRQKYSFNEHYKRFMLKPYESFEELTGKEMSALEALYGDIDAVEIYPALVKKRP 518  
 QY 499 RPDALFGETWVEVGFSLKGLMGVIVICSPAYWKSTGEGEVGOIINTASIOSLICNNV 558  
 DB 519 RPDALFGETWVEVGFSLKGLMGVIVICSPAYWKSTGEGEVGOIINTASIOSLICNNV 578  
 QY 559 KCCPFTSEVPPDELKIVTINASSRSGLDINPTVLKERTEL 604  
 DB 579 KCCPFTSEVPPDELKIVTINASSRSGLDINPTVLKERTEL 606

RESULT 14  
 ID 080V03 PRELIMINARY; PRT; 593 AA.  
 AC 080V03;  
 DT 01-MAR-2002 (TEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Cyclooxygenase.  
 OS Squalus acanthias (Spiny dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Squalidae; Squalus.  
 OC NCBI\_TaxID=7797;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Rectal gland;  
 RA Yang T., Forrest S., Stine N., Endo Y., Pasumaththy A., Aller S.,  
 RA Forrest J.N. Jr., Scherman J.B., Briggs J.P.;  
 RT "Cloning of a cyclooxygenase cDNA from dogfish shark, Squalus  
 RT acanthias, and its role in the regulation of rectal gland chloride  
 RT secretion";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF420317; ALU37727.1; -  
 DR GO: GO:0004601; F:peroxidase activity; IEA.  
 DR GO: GO:0006979; P:response to oxidative stress; IEA.  
 DR InterPro: IPR002007; Anim\_peroxidase.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR002016; peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR Pfam: PF00008; EGF; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR SMART: SM00181; EGF; 1.  
 DR PROSITE: PS50292; PEROXIDASE\_3; 1.  
 DR SEQUENCE 593 AA; 68274 MW; 85F2C870B04ED0F CRC64;

Query Match 63.1%; Score 2041.5; DB 13; Length 593;  
 Best Local Similarity 62.1%; Pred. No. 3e-157;  
 Matches 355; Conservative 101; Mismatches 111; Indels 5; Gaps 2;

QY 3 ARALL-----LCANLALSHTA-NPCSHPCQNRGVMSVGFDOYKCDCTRTGYGNCSTP 57  
 DB 4 ARILLLLPLCLPKADTTAINPCYYPQCKGICVNVGKEGECDCRTGYGVNCTPP 63  
 QY 58 EPLTRIKLPLKPTNTVHYILTFKGFMMVNNIPFLNAINSVYLTSSHLIDSPPTN 117  
 DB 64 FMSRVHFKLSPSSMHVILTHYKMLWIIINNISFSDTLMLVLTVANILPSPPTN 123  
 QY 118 ADYGYKSWAFNSLYTRALPVPDCEPTPLGVKKKQLPDSNEIVEKLLRRKPIPP 177  
 DB 124 SYTYVSWEGYSNISITLRLPVPKDCPTPTGQYKLLPDSQAEFLLRKRIIPP 183  
 QY 178 QGSNNMFAFFAOFHFOFKTDHKGPAFTNGLGHVLDLNIYGETLAKQRLKLPKQK 237  
 DB 184 QGSNNMFAFFAOFHFOFKTDHKGPAFTNGLGHVLDLNIYGETLAKQRLKLPKQK 243  
 QY 238 MKYQIIDGEMRPVYKDTQAEMLYRPVVEHLRFVAGQEVFGLVPGIMVYATITMLREHR 297  
 DB 244 LKQYVNGVPPSPYKXEARIQMKYPTSLDEKRLAIGHPTFGLIPELMMYATITMLREHR 303  
 QY 298 VCDVUKQEHPEWDEQLFQTSRLILGETIKIVIEDYVQHLSGYHFKLPDELLFNKQF 357  
 DB 304 VCDILKEHPVMSDEQLFQTSRLILGETIKIVIEDYVQHLSGYHFKLPDELLFNKQF 363  
 QY 358 QYONRIAAEFNTLYMHNPRLPDTQIHOQKYYQOFYNNLSLLEHGITQFVSESTRQIA 417  
 DB 364 QYONRIAAEFNTLYMHNPRLPDTQIHOQKYYQOFYNNLSLLEHGITQFVSESTRQIA 423  
 QY 418 GRVAGRVNPAVQKVASIDOSROMKYYQSFNEYKRFMLKPYSEFELTGEKMSAEI 477  
 DB 424 GRIGGRNIIHQSLHIAIATIEHGLLRFQRYNEIRKLLGLTPYKSFQELTGEREVAAEL 483  
 QY 478 EALYGDIDAVELYPALVEKRPDAIPSETWVEGAPFSLKGLMGNVICSPAYWKPSTFG 537  
 DB 484 EKLIGHIDAMEFYRALLLEAPNKNSIFGESWEMGAPFSLKGLMGNVICSPAYWKPSTFG 543  
 QY 538 GEVGFQINTASIOSLICNNVKGCFSTFSVP 569  
 DB 544 GKTGFQINTATFTEKILCLNVKCKPYGVGFHP 575

RESULT 15  
 ID 08JH44 PRELIMINARY; PRT; 597 AA.  
 AC 08JH44.  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Prostaglandin G/H synthase 1.  
 GN PRGSI.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NX NCBI\_TaxID=7955;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12011329;  
 RA Grosser T., Yusuf S., Cheskis E., Pack M.A., Fitzgerald G.A.;  
 RT "Developmental expression of functional cyclooxygenases in  
 zebrafish."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8418-8423(2002).  
 DR EMBL: AY028584; AAK31030.1; -  
 DR GO: GO:0004601; F:peroxidase activity; IEA.  
 DR GO: GO:0006979; P:response to oxidative stress; IEA.  
 DR InterPro: IPR002007; Anim\_peroxidase.  
 DR InterPro: IPR002016; peroxidase.  
 DR Pfam: PF03098; An\_peroxidase; 1.  
 DR PRINTS: PR00457; ANPEROXIDASE.  
 DR PROSITE: PS50292; PEROXIDASE\_3; 1.  
 DR SEQUENCE 597 AA; 68963 MW; A13593679926F292 CRC64;

Query Match 63.0%; Score 2040.5; DB 13; Length 597;  
 Best Local Similarity 64.7%; Pred. No. 3.6e-157;  
 Matches 359; Conservative 86; Mismatches 109; Indels 1; Gaps 1;

QY 15 SHTANPCSHPCQNRGVMSVGFDOYKCDCTRTGYGNCSTPEFLTRIKLFLKPYNTY 74  
 DB 30 SNTANPCCYYPQONOGICVRYGLERYECDCTRTGYGNCSTPEFLTRIKLFLKPYNTY 89  
 QY 75 HYILTFKGFMMVNNIPFLNAINSVYLTSSHLIDSPPTNADYGYKSWAFNSLY 134  
 DB 90 HYILTFKGFMMVNNIPFLNAINSVYLTSSHLIDSPPTNADYGYKSWAFNSLY 148  
 QY 135 TRALPVPDCEPTPLGVKKKQLPDSNEIVEKLLRRKIPPOGSNNMFAFFAOFHFO 194  
 DB 149 TRILPVPDCEPTPTMGTKIKLPDKLVEKMLRRNFRIDPOGNNMFAFFAOFHFO 208  
 QY 195 FPKTHKGPATNGLGHVLDLNIYGETLAKQRLKLPKQKMKYQIIDGEMRPVYK 254  
 DB 209 FPKTHKGPATNGLGHVLDLNIYGETLAKQRLKLPKQKMKYQIIDGEMRPVYK 268  
 QY 255 TQAEMLYRPVVEHLRFVAGQEVFGLVPGIMVYATITMLREHRVCDVUKQEHPEWDEQL 314  
 DB 269 TQAEMLYRPVVEHLRFVAGQEVFGLVPGIMVYATITMLREHRVCDVUKQEHPEWDEQL 328  
 QY 315 FQTSRLILGETIKIVIEDYVQHLSGYHFKLPDELLFNKQFQYONRIAAEFNTLYMH 374  
 DB 329 FQTSRLILGETIKIVIEDYVQHLSGYHFKLPDELLFNKQFQYONRIAAEFNTLYMH 388  
 QY 375 PLPPTQIHOQKYYQOFYNNLSLLEHGITQFVSESTRQIAGRVNPAVQKVAS 434  
 DB 389 PLPPTQIHOQKYYQOFYNNLSLLEHGITQFVSESTRQIAGRVNPAVQKVAS 448  
 QY 435 QASIDOSROMKYYQSFNEYKRFMLKPYSEFELTGEKMSAELEALYGDIDAVELYPAL 494  
 DB 449 ERVIVSEHLLQFPNEYKRFMLKPYSEFELTGEKMSAELEALYGDIDAVELYPAL 508  
 QY 495 VEKRPDAIPSETWVEGAPFSLKGLMGNVICSPAYWKPSTFGGEVGFQINTASIOS 554  
 DB 509 LEKTRPGAIVGESWEMGAPFSLKGLMGNVICSPAYWKPSTFGGEVGFQINTASIOS 568  
 QY 555 CNNVKGCFSTFSVP 569  
 DB 569 CLNTKWCPEYVSFHTP 583

Search completed: April 24, 2004, 07:21:03  
 Job time : 75 secs

Blank

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 07:22:17 ; Search time 12760 Seconds

(without alignments)  
11504.926 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387

Sequence: 1 GTCGAGAACTCTCTCAGCAG.....GATTAATAAAAAAAAAAG 3387

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_ba:\*
- 2: gb\_hlg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_da:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_scs:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_hlg\_hum:\*
- 31: em\_hlg\_inv:\*
- 32: em\_hlg\_other:\*
- 33: em\_hlg\_mus:\*
- 34: em\_hlg\_pln:\*
- 35: em\_hlg\_rtd:\*
- 36: em\_hlg\_mam:\*
- 37: em\_hlg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_hlg\_hum:\*
- 40: em\_hlg\_mus:\*
- 41: em\_hlg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3387	100.0	3387	6	124360
2	3385.4	100.0	3387	6	AX328834
3	3379	99.8	3387	6	AR380505
4	3379	99.8	3387	6	AX082878
5	3379	99.8	3387	6	HUMCYCLOX
6	3375.8	99.6	3387	6	AR029278
7	3374.2	99.6	3387	6	AR106720
8	3374.2	99.6	3387	6	AR202531
9	3215	94.9	3394	9	BC013734
10	3161.4	93.3	3362	9	HUMENDOSYN
11	3087	91.1	3669	9	AY151286
12	1912.2	56.5	3314	4	U97696
13	1810.2	53.4	1815	9	AY462100
14	1803.2	53.2	1834	6	AR055229
15	1803.2	53.2	1834	6	AR055235
16	1727.8	51.0	10997	9	HUMPTGS2
17	1727	51.0	9453	6	AX332842
18	1727	51.0	9453	6	HSU04636
19	1720.6	50.8	11449	9	AY229989
20	1720.6	50.8	12551	9	AY382629
21	1719	50.8	84412	9	HS973M2
22	1650.8	48.7	3398	4	AF027334
23	1650.4	48.7	3621	6	AY028563
24	1621.6	47.9	3509	6	AR411929
25	1621.6	47.9	3509	6	AR411930
26	1620	47.8	3632	6	AX082874
27	1605.2	47.4	3489	4	AF031698
28	1605	47.4	3498	4	AY044905
29	1583	46.7	3483	4	CAU68486
30	1552.2	45.8	2763	10	CPCOX2
31	1528.6	45.1	4152	6	AX306255
32	1528.6	45.1	4152	10	MUSGRIPEHS
33	1525.8	45.0	3986	6	AR029276
34	1525.8	45.0	3986	10	MUSPCSF
35	1476.6	43.6	1812	6	AR411931
36	1476.6	43.6	1812	6	AR411932
37	1446	42.7	2340	10	MUSPEHSB
38	1432.8	42.3	1984	10	AY065644
39	1431.8	42.3	4154	10	S67722
40	1431.8	42.3	4404	10	AF233596
41	1417	41.8	4154	10	RRU03389
42	1410.6	41.6	1825	4	AF047841
43	1379.8	40.7	1920	6	AR055228
44	1355.2	40.0	1827	10	RATCYLOX
45	1348.4	39.8	1815	10	RNU04300

ALIGNMENTS

RESULT 1  
LOCUS 124360  
DEFINITION Sequence 11 from patent US 5543297.  
ACCESSION 124360  
VERSION 124360.1 GI:1604230  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3387)  
AUTHORS Cromlish, W.A., Kennedy, B.P., O'Neill, G., Vickers, P.J., Wong, E. and Mancini, U.A.  
TITLE Human cyclooxygenase-2 cDNA and assays for evaluating cyclooxygenase-2 activity

Pred. No. is the number of results predicted by chance to have a



QY 2041 GAGAAAGAGTCACTCTTGGAGACTTTTATGTCACTACTTAAGATTTTGGCTGTGC 2100  
 DB 2041 GAGAAAGAGTCACTCTTGGAGACTTTTATGTCACTACTTAAGATTTTGGCTGTGC 2100  
 QY 2101 TGTAAAGTTGAAAAAGTTTTTATCTGTTTATTAACCAAGAGAAATGAGTTTGA 2160  
 DB 2101 TGTAAAGTTGAAAAAGTTTTTATCTGTTTATTAACCAAGAGAAATGAGTTTGA 2160  
 QY 2161 CGTCTTTTAACTTGAATTTCACTTATATTAAGAGCAAGAGTAAGATGTTTGAATAC 2220  
 DB 2161 CGTCTTTTAACTTGAATTTCACTTATATTAAGAGCAAGAGTAAGATGTTTGAATAC 2220  
 QY 2221 TTAAAGCTATGCAAGATGCGCAAAATGCTGAAAGTTTAACTGTGATGTTTCCAT 2280  
 DB 2221 TTAAAGCTATGCAAGATGCGCAAAATGCTGAAAGTTTAACTGTGATGTTTCCAT 2280  
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 REFERENCE  
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 AUTHORS Cromlish W.A., Kennedy B.P., O'Neill G., Vickers P.J., Wong E. and Mancini J.A.  
 TITLE Assay for evaluating inhibition of cyclooxygenase-2  
 JOURNAL Patent: EP 1130110-A 11 05-SEP-2001; Merck Frost Canada & Co. (CA)  
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Db	1921	TGATCATATTTATTTATTTATATGAACCATGTCATTAATTTATTTATTAATAATTT	1980
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 TITLE Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.  
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VERSION     AX082878.1  GI:13184807
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AUTHORS     Gierse, J.K.
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Qy	2041	GAGAAAGAGTCACTACTGTGGAAGCTTTTATGTCACTACCTAAAGATTTTGTCTGTGC	2100

Db	2041	GAGAAAGAGTCATCTCTGGGAAGCTTTATATGCTACCTGATCTAAAGATTTTGCTGTCC	2100
Qy	2101	TGTTAAGTTGGAAAACAGTTTTTATCTGTGTTTTATTAACACAGAGAAATGAGTTTTA	2160
Db	2101	TGTTAAGTTGGAAAACAGTTTTTATCTGTGTTTTATTAACACAGAGAAATGAGTTTTA	2160
Qy	2161	CGCTCTTTTACTTGAATTTTCAACTATATATAAGACGAAATGATGTTGAATAC	2220
Db	2161	CGCTCTTTTACTTGAATTTTCAACTATATATAAGACGAAATGATGTTGAATAC	2220
Qy	2221	TTAAACACTATACAAAGATGCGAAATGCTGAAGTTTTTACCTGTCATGTTTCCAT	2280
Db	2221	TTAAACACTATACAAAGATGCGAAATGCTGAAGTTTTTACCTGTCATGTTTCCAT	2280
Qy	2281	GCATCTTCATGATGCAATGGAAGTAACTATAGTTTGAATTTTAAAGTCTTTGGGTA	2340
Db	2281	GCATCTTCATGATGCAATGGAAGTAACTATAGTTTGAATTTTAAAGTCTTTGGGTA	2340
Qy	2341	TTTTTCTGTCCAAACAAACAGGATCAGTGCAATTTATTAATGAATTTAAATTAGA	2400
Db	2341	TTTTTCTGTCCAAACAAACAGGATCAGTGCAATTTATTAATGAATTTAAATTAGA	2400
Qy	2401	CATTACCGATATTTCATGCTACTCTTTTAAATCAGACANAGAACTAATTGAAAT	2460
Db	2401	CATTACCGATATTTCATGCTACTCTTTTAAATCAGACANAGAACTAATTGAAAT	2460
Qy	2461	TCTAATTCATAGGGTAGAATCACCCTGTAAAGCTGTTGATTTCTTAAAGTATTAA	2520
Db	2461	TCTAATTCATAGGGTAGAATCACCCTGTAAAGCTGTTGATTTCTTAAAGTATTAA	2520
Qy	2521	CTTGATACATPACCAAAAAGAGCTGTCTGGATTTAAATCTGTAAATCAGATGAAAT	2580
Db	2521	CTTGATACATPACCAAAAAGAGCTGTCTGGATTTAAATCTGTAAATCAGATGAAAT	2580
Qy	2581	TTACTACAAATGCTGTTAAATAATTTATAAGTAGATGCTCTTTCACCAAGATATA	2640
Db	2581	TTACTACAAATGCTGTTAAATAATTTATAAGTAGATGCTCTTTCACCAAGATATA	2640
Qy	2641	AACTTTTAAGTGACTGTGTAACCTTCCTTTTAATCAAAATGCGAATTTATTAAG	2700
Db	2641	AACTTTTAAGTGACTGTGTAACCTTCCTTTTAATCAAAATGCGAATTTATTAAG	2700
Qy	2701	TGCTGAGCACTGAGAGTATATCCAAATTAAGAAATCTGTTGAGATTCAGAAAT	2760
Db	2701	TGCTGAGCACTGAGAGTATATCCAAATTAAGAAATCTGTTGAGATTCAGAAAT	2760
Qy	2761	CTGTTATATGCTGTGAACATGTAAACCCCATPACCCGCAAAAGGGGTCCTACCC	2820
Db	2761	CTGTTATATGCTGTGAACATGTAAACCCCATPACCCGCAAAAGGGGTCCTACCC	2820
Qy	2821	TTGACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTAAGGT	2880
Db	2821	TTGACATTAAGCAATTAACCAAGAGAAAGCCCAATTTATGTTCCAAATTAAGGT	2880
Qy	2881	TTAAACTTTTAAAGCAACTTTTAAAGCTTTGACCTTGACAGCAGACTGTACTCAGAT	2940
Db	2881	TTAAACTTTTAAAGCAACTTTTAAAGCTTTGACCTTGACAGCAGACTGTACTCAGAT	2940
Qy	2941	TTTGCTATAGGTTAATGAAGTACAGAGCTGTGCTTGAATACGATATGTTTCTCAGAT	3000
Db	2941	TTTGCTATAGGTTAATGAAGTACAGAGCTGTGCTTGAATACGATATGTTTCTCAGAT	3000
Qy	3001	TTTCTGTCTACAGTTAATTTAGACAGTCCATATCAGATGCGAAAGTAGCAATGACCTC	3060
Db	3001	TTTCTGTCTACAGTTAATTTAGACAGTCCATATCAGATGCGAAAGTAGCAATGACCTC	3060
Qy	3061	ATAAAATACCTCTTCAAAATGCTTAAATCATTTACACATTAATTTATCTCAGTCTTG	3120
Db	3061	ATAAAATACCTCTTCAAAATGCTTAAATCATTTACACATTAATTTATCTCAGTCTTG	3120
Qy	3121	AAAGCAATTCAGTAGTGATTTAGAAATCAAGCTGGCTAACCTGCATGCTGTTCCCTTCT	3180
Db	3121	AAAGCAATTCAGTAGTGATTTAGAAATCAAGCTGGCTAACCTGCATGCTGTTCCCTTCT	3180

QY	3181	TTTCTCTTTTAGCATTTTGGCTAAAGACAGACAGTCTTCCAAACACTTGTTCTCTCA	3240
Db	3181	TTTCTCTTTTAGCCATTTTGTCTAAGACACACAGTCTTCCAAACACTTGTTCTCTCA	3240
QY	3241	TTTGTGTTTACTAGTTTAAAGATCAGAGTTCACCTTTCTTGGACCTGCTCATATTTTCT	3300
Db	3241	TTTGTGTTTACTAGTTTAAAGATCAGAGTTCACCTTTCTTGGACCTGCTCATATTTTCT	3300
QY	3301	TACTGAACTTTTGCAAGTTTTCAGGTAAACCTGAGCTCAGACTGCAATTAGCTCTC	3360
Db	3301	TACTGAACTTTTGCAAGTTTTCAGGTAAACCTGAGCTCAGACTGCAATTAGCTCTC	3360
QY	3361	TTAAGAGATTAAAAAAG 3387	
Db	3361	TTAAGAGATTAAAAAAG 3387	
RESULT 7			
	AR106720	3387 bp	DNA
	LOCUS		linear
	DEFINITION	Sequence 19 from patent US 6107087.	PAT 14-FEB-2001
	ACCESSION	AR106720	
	VERSION	AR106720.1	GI:12821250
	KEYWORDS		
	SOURCE	Unknown.	
	ORGANISM	Unknown.	
	REFERENCE	Unclassified.	
	AUTHORS	1 (bases 1 to 3387)	
	TITLE	O'Neill, G.P. and Mancini, J.A.	
	JOURNAL	High level expression of human cyclooxygenase-2	
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		/mol_type="unassigned DNA"	
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	Best Local Similarity	99.8%; Pred. No. 0;	
	Matches 3379; Conservative	0; Mismatches 8; Indels 0; Gaps 0;	
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Db	1	GTCCAGAACTCTCTCAGACAGCGCTCTTCAAGCTCCACAGCGCGCTCAGACAGCA	60
QY	61	AAGCTTACCCCGCGCGCGCGCTCTGCGCGCTGCGCGCTGCGCTGCGCTGCGCT	120
Db	61	AAGCTTACCCCGCGCGCGCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCTGCGCT	120
QY	121	GTGCGCGGTCTGAGCGCTCAGCCATACAGCAATCTTGCTGTTCCACCCATGTCAAA	180
Db	121	GTGCGCGGTCTGAGCGCTCAGCCATACAGCAATCTTGCTGTTCCACCCATGTCAAA	180
QY	181	CCGAGTGTATATAGAGTGTGGATTGACACAGTAAAGTGCATTTGACCCGACAG	240
Db	181	CCGAGTGTATATAGAGTGTGGATTGACACAGTAAAGTGCATTTGACCCGACAG	240
QY	241	ATTCTATGAGAAAATGCTCAACACCGAATTTTGTGACAGAAATTAATTTTCTGAA	300
Db	241	ATTCTATGAGAAAATGCTCAACACCGAATTTTGTGACAGAAATTAATTTTCTGAA	300
QY	301	ACCCACTCCAAACAGTGCATCAATCTTACCCACTTCAAGGATTTTGAAGTTGT	360
Db	301	ACCCACTCCAAACAGTGCATCAATCTTACCCACTTCAAGGATTTTGAAGTTGT	360
QY	361	GAAATACATTCCTCTTCCGAAAGTCAATTTGATTTGTTGATGACATCCAGATCA	420
Db	361	GAAATACATTCCTCTTCCGAAAGTCAATTTGATTTGTTGATGACATCCAGATCA	420
QY	421	TTTGATTTGACAGTCCACCAATTAATCAATCTGATATGCTTCAAAAGCTGGAGCTT	480
Db	421	TTTGATTTGACAGTCCACCAATTAATCAATCTGATATGCTTCAAAAGCTGGAGCTT	480



QY	481	CTCTAACTCTCTTATTAATCTAGAGCCCTTCTCTCTGCTCATGATTTGCCGACCTC	540
Db	481	CTCTAACTCTCTTATTAATCTAGAGCCCTTCTCTCTGCTCATGATTTGCCGACCTC	540
QY	541	CTTGGGCTCAAAAGTTAAAGAGAGCTTCTGATTTCAATGAGATTGTGAAAATTTGCT	600
Db	541	CTTGGGCTCAAAAGTTAAAGAGAGCTTCTGATTTCAATGAGATTGTGAAAATTTGCT	600
QY	601	TTTAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAACATGATGTTTGCAATCTTTG	660
Db	601	TTTAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAACATGATGTTTGCAATCTTTG	660
QY	661	CCAGGACTTCAGGCAACGATTTTCAAGACATCATTAAGCAGGCGCAGCTTTCACTAA	720
Db	661	CCAGGACTTCAGGCAACGATTTTCAAGACATCATTAAGCAGGCGCAGCTTTCACTAA	720
QY	721	CGGGCTGGGCAATGGGGTGAATTAAATATTAATGAGTAACTGGGCTGAGACAGG	780
Db	721	CGGGCTGGGCAATGGGGTGAATTAAATATTAATGAGTAACTGGGCTGAGACAGG	780
QY	781	TAAATCTGGCTTTTCAAGATGAGAAAAATGAATATCAGATTAATGATGAGAGATGA	840
Db	781	TAAATCTGGCTTTTCAAGATGAGAAAAATGAATATCAGATTAATGATGAGAGATGA	840
QY	841	TCTCTCCCAAGTCAAAAGATCTCAGGACAGAGATGATCTTCTCTCAAGTCTCTGAGCA	900
Db	841	TCTCTCCCAAGTCAAAAGATCTCAGGACAGAGATGATCTTCTCTCAAGTCTCTGAGCA	900
QY	901	TTTACGGTTTGTGTGGGACAGAGAGTCTTTGGTCTGGTCTGGTCTGATGATATATATGC	960
Db	901	TTTACGGTTTGTGTGGGACAGAGAGTCTTTGGTCTGGTCTGGTCTGATGATATATATGC	960
QY	961	CACAAATCTGGGCTGGGAAACACAAAGAGATGATGATGCTTTAAACAGAGACATCTGA	1020
Db	961	CACAAATCTGGGCTGGGAAACACAAAGAGATGATGATGCTTTAAACAGAGACATCTGA	1020
QY	1021	ATGGGGTATGAGAGTGTTCACAGACAGAGGCTAATACGATGAGAGAGACATATTA	1080
Db	1021	ATGGGGTATGAGAGTGTTCACAGACAGAGGCTAATACGATGAGAGAGACATATTA	1080
QY	1081	GATTGTGATGAGATTAATGTGCAACACTTGAAGGCTATCACTTCAAACTGAAATTTGA	1140
Db	1081	GATTGTGATGAGATTAATGTGCAACACTTGAAGGCTATCACTTCAAACTGAAATTTGA	1140
QY	1141	CCGAGACATCTTTCAACAAACATTCAGATCCAAATGCTATTTGCTGCTGAATTTAA	1200
Db	1141	CCGAGACATCTTTCAACAAACATTCAGATCCAAATGCTATTTGCTGCTGAATTTAA	1200
QY	1201	CACCTCTATCACTGGACATCCCTCTGTGCTGACACCTTCAAAATCATGACAGAAATA	1260
Db	1201	CACCTCTATCACTGGACATCCCTCTGTGCTGACACCTTCAAAATCATGACAGAAATA	1260
QY	1261	CAACTATCAAGTTTATCTAACAACTCTATATTTGCTGGAATGGAATTTACCCAGTT	1320
Db	1261	CAACTATCAAGTTTATCTAACAACTCTATATTTGCTGGAATGGAATTTACCCAGTT	1320
QY	1321	TGTTGAATCATTCACAGGCAAAATTTGCTGCAAGGTTGCTGCTGATGGAATGTTCCACC	1380
Db	1321	TGTTGAATCATTCACAGGCAAAATTTGCTGCAAGGTTGCTGCTGATGGAATGTTCCACC	1380
QY	1381	CGCAGTACAGAAAGTATCAAGGCTTCCATTGACCAAGCAGGCAAGTGAATATCACAGTC	1440
Db	1381	CGCAGTACAGAAAGTATCAAGGCTTCCATTGACCAAGCAGGCAAGTGAATATCACAGTC	1440
QY	1441	TTTTAAATGAGTACCGCAAAAGCTTTATGCTGAGAGCCTATGAAATCATTTGAAGAACTTAC	1500
Db	1441	TTTTAAATGAGTACCGCAAAAGCTTTATGCTGAGAGCCTATGAAATCATTTGAAGAACTTAC	1500
QY	1501	AGGAGAAAAGAAATGTCTGACAGGTTGGAAGCACTCTATGCTGACATGATCTGTGGA	1560
Db	1501	AGGAGAAAAGAAATGTCTGACAGGTTGGAAGCACTCTATGCTGACATGATCTGTGGA	1560
QY	1561	GCTGATCTGCGCTCTGAGTGAAGAAAGCCTCGGCAATGCAATCTTTGGTGAACCAT	1620
Db	1561	GCTGATCTGCGCTCTGAGTGAAGAAAGCCTCGGCAATGCAATCTTTGGTGAACCAT	1620
QY	1621	GGTAAAGTTGAGACCACTTCTCTTGAAGAGCTTAAGGGTATGTTATATGTTCTCC	1680
Db	1621	GGTAAAGTTGAGACCACTTCTCTTGAAGAGCTTAAGGGTATGTTATATGTTCTCC	1680
QY	1681	TGCTTACTGGAAGCCAGACATTTTGGTGGAAAGTGGGTTTCAAAATCATCAACATGCG	1740
Db	1681	TGCTTACTGGAAGCCAGACATTTTGGTGGAAAGTGGGTTTCAAAATCATCAACATGCG	1740
QY	1741	CTCAATTCAGTCTCTCATCTGCAATTAAGGAAGGCTGTCCTTCACTTCACTCATGCT	1800
Db	1741	CTCAATTCAGTCTCTCATCTGCAATTAAGGAAGGCTGTCCTTCACTTCACTCATGCT	1800
QY	1801	TCGATTCAGAGCTCATTAATAACAGTCAACATCATGCAAGTTCTTCCGCTCGGACT	1860
Db	1801	TCGATTCAGAGCTCATTAATAACAGTCAACATCATGCAAGTTCTTCCGCTCGGACT	1860
QY	1861	AGATGATATCAATCCCACTACTACTTAAAGAAAGCGTCACTGAACTGTGAAGTCTAA	1920
Db	1861	AGATGATATCAATCCCACTACTACTTAAAGAAAGCGTCACTGAACTGTGAAGTCTAA	1920
QY	1921	TGATCATATTTATTTATTAATGAACCAAGTCAATTAATTTATTAATTAATTTT	1980
Db	1921	TGATCATATTTATTTATTAATGAACCAAGTCAATTAATTTATTAATTAATTTT	1980
QY	1981	ATATTAACCTCTTATGTTACTTAACATCTTCTGTAACAGAGTCACTGCTGTTGCG	2040
Db	1981	ATATTAACCTCTTATGTTACTTAACATCTTCTGTAACAGAGTCACTGCTGTTGCG	2040
QY	2041	GAGAAAGAGTCAATCTTGTGAAGACCTTATGCTCACTCAATTAAGATTTGCTGTGC	2100
Db	2041	GAGAAAGAGTCAATCTTGTGAAGACCTTATGCTCACTCAATTAAGATTTGCTGTGC	2100
QY	2101	TGTTAAAGTTGGAAGACGTTTATTTCTGTTTATTAACAGAGAGAAATGAGTTTGA	2160
Db	2101	TGTTAAAGTTGGAAGACGTTTATTTCTGTTTATTAACAGAGAGAAATGAGTTTGA	2160
QY	2161	CGTCTTTTACTGGAATTTCACTTATTAATTAATGAAGCAAGAAATGATGTTGAATAC	2220
Db	2161	CGTCTTTTACTGGAATTTCACTTATTAATTAATGAAGCAAGAAATGATGTTGAATAC	2220
QY	2221	TTAAACATATCAAGATGCCAAATGCTGAAAGTTTATACAGTGTGATGTTCCAAAT	2280
Db	2221	TTAAACATATCAAGATGCCAAATGCTGAAAGTTTATACAGTGTGATGTTCCAAAT	2280
QY	2281	GCATCTTCATGATGATTAAGAGTACTTAATGTTTGAATTTTAAAGTACTTTGGGATA	2340
Db	2281	GCATCTTCATGATGATTAAGAGTACTTAATGTTTGAATTTTAAAGTACTTTGGGATA	2340
QY	2341	TTTTCTGTCAACAAACAAACAGGATACGATGATTAATTAATGAATTTAAATTTAA	2400
Db	2341	TTTTCTGTCAACAAACAAACAGGATACGATGATTAATTAATGAATTTAAATTTAA	2400
QY	2401	C	

Db	2641	AAACCTTTTATGTTGACTGCTTTAAAACCTTCTTTTAAATCAAAATGCCAAATTATTAAAGS	2700
QY	2701	TGGTGGAGCAGCTGCACTGTTATCTCAAAATTAAGATATCCTGTGGAGATATTCCGAAT	2760
Db	2701	TGGTGGAGCAGCTGCACTGTTATCTCAAAATTAAGATATCCTGTGGAGATATTCAGAAAT	2760
QY	2761	CTGTGTTATATGGCTGGTGAACATGTGTAACCCCATATACCCCGCCAAAAGGGGCTCTAACCC	2820
Db	2761	CTGTGTTATATGGCTGGTGAACATGTGTAACCCCATATACCCCGCCAAAAGGGGCTCTAACCC	2820
QY	2821	TTGAAACATTAAGCAATATACCAAGAGAAAAAGCCCAATTATGTGTTCCAAATTTAGGGT	2880
Db	2821	TTGAAACATTAAGCAATATACCAAGAGAAAAAGCCCAATTATGTGTTCCAAATTTAGGGT	2880
QY	2881	TTTAAACTTTTGAAGCAAACTTTTTTTATAGCCTGTGACATCGACAGACCTGATCTAGAT	2940
Db	2881	TTTAAACCTTTTGAAGCAAACTTTTTTTATAGCCTGTGACATCGACAGACCTGATCTAGAT	2940
QY	2941	TTTGTCTATGAGGTTAATGAAGTACCAAGCTGTGCTGATATACGATAATGTTTTCTCAGAT	3000
Db	2941	TTTGTCTATGAGGTTAATGAAGTACCAAGCTGTGCTGATATACGATAATGTTTTCTCAGAT	3000
QY	3001	TTTCTGTGTGTAACGTTTAATTATAGCAGTCCATATCACTTGACAAAAGTAGCAATGACCTC	3060
Db	3001	TTTCTGTGTGTAACGTTTAATTATAGCAGTCCATATCACTTGACAAAAGTAGCAATGACCTC	3060
QY	3061	ATTAAATATACCTCTCAAAATGCTTAAATCTATTTCAACATTTAATTTATCTCAGCTCTG	3120
Db	3061	ATTAAATATACCTCTCTCAAAATGCTTAAATCTATTTCAACATTTAATTTATCTCAGCTCTG	3120
QY	3121	AAGCCAAATCAGTAGTGATGATGGAATCAGACCTGTGCTACCTGCAATGTCTGTTCTTTCT	3180
Db	3121	AAGCCAAATCAGTAGTGATGATGGAATCAGACCTGTGCTACCTGCAATGTCTGTTCTTTCT	3180
QY	3181	TTTCTCTCTTTTGAAGCATTTTGCTTAAGACACAGCATCTTCCAAAACACTGCTTCTCCTTA	3240
Db	3181	TTTCTCTCTTTTGAAGCATTTTGCTTAAGACACAGCATCTTCCAAAACACTGCTTCTCCTTA	3240
QY	3241	TTTGTGTTTACAGTTTAAAGATCAGAGTTCACTTTCTTTGGACTGTGCTTAATATTTCT	3300
Db	3241	TTTGTGTTTACAGTTTAAAGATCAGAGTTCACTTTCTTTGGACTGTGCTTAATATTTTCT	3300
QY	3301	TACCTGAACCTTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGCTGCTATTTAGTCTCTC	3360
Db	3301	TACCTGAACCTTTTGCAAGTTTTCAGGTAAACCTCAGCTCAGAGCTGCTATTTAGTCTCTCTC	3360
QY	3361	TTAAGAAAGTATTAAGAAAAAAGAAAAAAG 3387	
Db	3361	TTAAGAAAGTATTAAGAAAAAAGAAAAAAG 3387	

Query Match	Score	DB	Length
99.6%;	3374.2;	DB 6;	3387;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3379; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	I	GTCCAGGAATCCTCCAGACGCGCTCCTTCAAGTCCAGACGCCAGAGCCCTCAGACAGA	60
Db	1	GTCCAGGAATCCTCCAGACGCGCTCCTTCAAGTCCAGACGCCAGAGCCCTCAGACAGA	60
QY	61	AAGGCTACCCCGCGCGCGCCCTGCGCGCGCTGCGAGTCTGCGCCCTGCTGCT	120
Db	61	AAGGCTACCCCGCGCGCGCCCTGCGCGCGCTGCGAGTCTGCGCGCGCCCTGCTGCT	120
QY	121	GTGGCGGCTCTGGCGCTCAGGCATACAGAAATCCTGCTGTCCACCAATGTCAAA	180
Db	121	GTGGCGGCTCTGGCGCTCAGGCATACAGAAATCCTGCTGTCCACCAATGTCAAA	180
QY	181	CCGAGGTGTATGTATAGTGTGGGATTTGACAGTAAAGTCGATTTGACCGGACAG	240
Db	181	CCGAGGTGTATGTATAGTGTGGGATTTGACAGTAAAGTCGATTTGACCGGACAG	240
QY	241	ATTCTATAGGAAAAACGTCCACACCCGAAATTTTGAACAAGATTAATTTCTGAA	300
Db	241	ATTCTATAGGAAAAACGTCCACACCCGAAATTTTGAACAAGATTAATTTCTGAA	300
QY	301	ACCACTCCAAACACAGTGCATACATCTTACCACTTCGAAAGGATTTTGAACTGT	360
Db	301	ACCACTCCAAACACAGTGCATACATCTTACCACTTCGAAAGGATTTTGAACTGT	360
QY	361	GAATPACATTTCCCTCTCTTGAAATGCAATTAAGTATAGTGTACATCCGATCA	420
Db	361	GAATPACATTTCCCTCTCTTGAAATGCAATTAAGTATAGTGTACATCCGATCA	420
QY	421	TTTATATGACAGTCCACCACTTACAAATGCTGACTATGCTCAAAAAGCTGGAACTTT	480
Db	421	TTTATATGACAGTCCACCACTTACAAATGCTGACTATGCTCAAAAAGCTGGAACTTT	480
QY	481	CTCTPACCTCTCTTATTAATACAGAGCCCTTCTCTCTGCGCGATGATTTGCCGACTCC	540
Db	481	CTCTPACCTCTCTTATTAATACAGAGCCCTTCTCTCTGCGCGATGATTTGCCGACTCC	540
QY	541	CTGGGCTCAAGAGTAAAGACGCTCTGATTTCAATAGATTTGTGAAAAATTTGCT	600
Db	541	CTGGGCTCAAGAGTAAAGACGCTCTGATTTCAATAGATTTGTGAAAAATTTGCT	600
QY	601	TCTAAGAAAGAAATTCATCCCTGATCCCGACGCGCTCAACATGATTTTGTATTTCTTGC	660
Db	601	TCTAAGAAAGAAATTCATCCCTGATCCCGACGCGCTCAACATGATTTTGTATTTCTTGC	660
QY	661	CCAGACTTCACAGACCAAGTTTTCAGACAGATCATTAAGGAGAGGCGAGTTTCAACAA	720
Db	661	CCAGACTTCACAGACCAAGTTTTCAGACAGATCATTAAGGAGAGGCGAGTTTCAACAA	720
QY	721	CGGGCTGGGCGCATGGGGTGACTTAATCATATTTACGTGAAACTCTGCTAGACGCG	780
Db	721	CGGGCTGGGCGCATGGGGTGACTTAATCATATTTACGTGAAACTCTGCTAGACGCG	780
QY	781	TAAACTGGGCTTTTCAAGGATGAAAAATGAAATATACGATTAATTTGATGAGAGATGA	840
Db	781	TAAACTGGGCTTTTCAAGGATGAAAAATGAAATATACGATTAATTTGATGAGAGATGA	840
QY	841	TCTCTCCACAGTCAAAAGTACTCAGGCGAGATGATCTACCTCTCGTAAGTCCCTGAGCA	900
Db	841	TCTCTCCACAGTCAAAAGTACTCAGGCGAGATGATCTACCTCTCGTAAGTCCCTGAGCA	900
QY	901	TCTACGCTTTGCTGTGGGCGAGAGAGTCTTTGTGCTGGTGTGCTGATGATGATATGC	960
Db	901	TCTACGCTTTGCTGTGGGCGAGAGAGTCTTTGTGCTGGTGTGCTGATGATGATATGC	960
QY	961	CACAATCTGGCTGGCGGAACAAACAGAGTATGCGATGCTTAAACGAGGAGCTCTCGA	1020
Db	961	CACAATCTGGCTGGCGGAACAAACAGAGTATGCGATGCTTAAACGAGGAGCTCTCGA	1020
QY	1021	ATGGGCTGATAGCAGTTGTTCCAGACAAACAGGCTAATCTGATAGAGAGATATTTAA	1080

Db 1021 ATGGGATGATGAGCAGTTGTTCCAGACAGAGCCTAACTGATAGAGACTATTTAA 1080  
QY 1081 GATTGATATGAGATTAATGTCGACAACTTGAGTGGCTATCACTTCAACCTGAATTTGA 1140  
Db 1081 GATTGATATGAGATTAATGTCGACAACTTGAGTGGCTATCACTTCAACCTGAATTTGA 1140  
QY 1141 CCCGAACTACTTTTGAACAAACAAATCCAGTACCAAAATCGTATTTGCTGCTGAATTTAA 1200  
Db 1141 CCCGAACTACTTTTGAACAAACAAATCCAGTACCAAAATCGTATTTGCTGCTGAATTTAA 1200  
QY 1201 CACCTCTATCACTGAGTACCCCTCTGCTGACACCTTCAATTCATGACGAGAAATA 1260  
Db 1201 CACCTCTATCACTGAGTACCCCTCTGCTGACACCTTCAATTCATGACGAGAAATA 1260  
QY 1261 CAACCTATCAACAGTTTATCTACAAACAACTCTATTTGCTGGAATGGAATTTCCAGTT 1320  
Db 1261 TGTATGATCAATTCACCAAGCAATGCTGCAAGGTTGCTGCTGATGGAATTTCCAGTT 1320  
QY 1321 TGTATGATCAATTCACCAAGCAATGCTGCAAGGTTGCTGCTGATGGAATTTCCAGTT 1380  
Db 1321 TGTATGATCAATTCACCAAGCAATGCTGCAAGGTTGCTGCTGATGGAATTTCCAGTT 1380  
QY 1381 CCGAGTACAGAAAGTATCAACAGGCTTCCATTGACACAGAGCAGATGGAATTAACAGTC 1440  
Db 1381 CCGAGTACAGAAAGTATCAACAGGCTTCCATTGACACAGAGCAGATGGAATTAACAGTC 1440  
QY 1441 TTTTATGATACCGCAAAAGCTTTATGCTGAAGCCCTATGAATCAATTTGAACACTTAC 1500  
Db 1441 TTTTATGATACCGCAAAAGCTTTATGCTGAAGCCCTATGAATCAATTTGAACACTTAC 1500  
QY 1501 AGAGAGAAAGAAATGCTGCAAGAGTTGGAAGACCTCTATGCTGACATGATGCTGTGA 1560  
Db 1501 AGAGAGAAAGAAATGCTGCAAGAGTTGGAAGACCTCTATGCTGACATGATGCTGTGA 1560  
QY 1561 GCTGTATCCTGCTCTCTGCTGAGAAAGCCTGCGCAGATGCCATTTTGGTGAACCAT 1620  
Db 1561 GCTGTATCCTGCTCTCTGCTGAGAAAGCCTGCGCAGATGCCATTTTGGTGAACCAT 1620  
QY 1621 GGTAGAAAGTTGAGACCACTTCTCTTGAAGGACTTATGAGTAAATGTTATGTTCTCC 1680  
Db 1621 GGTAGAAAGTTGAGACCACTTCTCTTGAAGGACTTATGAGTAAATGTTATGTTCTCC 1680  
QY 1681 TSCCTACTGGAAGCCAGACCTTTGCTGGAAGGCTGCTCCCTTACTTCACTTCACTGCT 1740  
Db 1681 TSCCTACTGGAAGCCAGACCTTTGCTGGAAGGCTGCTCCCTTACTTCACTTCACTGCT 1740  
QY 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCCCTTACTTCACTTCACTGCT 1800  
Db 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCCCTTACTTCACTTCACTGCT 1800  
QY 1801 TCCAGATCCAGAGCTCATTTAAACAGTCCATCAATGCAATGCTTCCCGCTCCGAGCT 1860  
Db 1801 TCCAGATCCAGAGCTCATTTAAACAGTCCATCAATGCAATGCTTCCCGCTCCGAGCT 1860  
QY 1861 AGATGATATCAATCCACAGTACTCTAATAAGAGGCTGCTGATGAACTGTAAAGTCTTA 1920  
Db 1861 AGATGATATCAATCCACAGTACTCTAATAAGAGGCTGCTGATGAACTGTAAAGTCTTA 1920  
QY 1921 TGAATCATATTTATTTATTAATGAACATGCTATTAATTTATTTATTTATTTATTTATTT 1980  
Db 1921 TGAATCATATTTATTTATTAATGAACATGCTATTAATTTATTTATTTATTTATTTATTT 1980  
QY 1981 ATATTTAACTCTTTATGTTACTTAAACATCTTCTGTAACAGAGTCACTCCGTTGCG 2040  
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TITLE	Human and mouse CDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903	(2002)
MEDLINE	22388257		
PUBMED	1247932		
REFERENCE	2	(bases 1 to 3394)	
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
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Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
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 VERSION U15326.1 GI:291987  
 KEYWORDS endoperoxide synthase type II.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3362)  
 Jones, D.A., Carlton, D.P., McIntyre, T.M., Zimmerman, G.A. and Prescott, S.M.  
 Molecular cloning of human prostaglandin endoperoxide synthase type II and demonstration of expression in response to cytokines  
 J. Biol. Chem. 268 (12), 9049-9054 (1993)  
 MEDLINE 93232069  
 PUBMED 8473346  
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## CDS

## ORIGIN

Query Match 93.3%; Score 3161.4; DB 9; Length 3362;  
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 Matches 3292; Conservative 0; Mismatches 66; Indels 21; Gaps 7;

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 VERSION AY151286.1 GI:24430027  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 3669)  
 AUTHORS Duan, Y.

## TITLE

Direct Submission

## JOURNAL

Submitted (18-SEP-2002) Department of Pathophysiology, Key  
 Laboratory of Pulmonary Disease of Ministry of Health, Tongji  
 Medical College, Huazhong University of Science and Technology,  
 Hangkong Road 13, Wuhan, Hubei 430030, China

## FEATURES

source

1. 3669

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## ORIGIN

Query Match

91.1%; Score 3087; DB 9; Length 3669;

Best Local Similarity 92.2%; Pred. No. 0;

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RESULT 12
LOCUS      U97696      3314 bp      mRNA      linear      MAM 25-SEP-1997
DEFINITION Oryctolagus cuniculus cyclooxygenase-2 (COX-2) mRNA, complete cds.
ACCESSION  U97696
VERSION     U97696.1 GI:2109296
KEYWORDS
SOURCE      Oryctolagus cuniculus (rabbit)
ORGANISM    Oryctolagus cuniculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1 (bases 1 to 3314)
            Guan,Y., Chang,M., Cho,W., Zhang,Y., Redha,R., Davis,L., Chang,S.,

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TITLE      Dubois,R.N., Hao,C.M. and Breyer,M.
            Cloning, expression, and regulation of rabbit cyclooxygenase-2 in
            renal medullary interstitial cells
JOURNAL    Am. J. Physiol. 273 (1 Pt 2), F18-F26 (1997)
MEDLINE    97393071
PUBMED     9249588
AUTHORS     Guan,Y., Chang,M., Cho,W., Zhang,Y., Redha,R., Davis,L., Chang,S.,
            Dubois,R.N., Hao,C.M. and Breyer,M.D.
TITLE      Direct Submission
JOURNAL    Submitted (15-APR-1997) Nephrology, Vanderbilt University Medical
            Center, Nashville, TN 37232-2372, USA
FEATURES
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## ORIGIN

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Query Match      56.5%; Score 1912.2; DB 4; Length 3314;
Best Local Similarity 78.6%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 618; Indels 99; Gaps 25;

Qy      59 CAAAGCTTACCCCGGCGGCGCTGCGCGCTGCGATGCTCGCCGCGCTGCTG 118
Db      16 CAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 75
Qy      119 CTGTGCGCGGCTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 178
Db      76 CTGTGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 135
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Qy      299 AAACCACTTCAAAACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 358
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Qy	1058	ATATCTGATGAGAGACTATTAAGATTTGATTTAAGATTTATGTCACACATTTGAGTGGC	1117
Db	961	ATATCTGATGAGAGACTATTAAGATTTGATTTAAGATTTATGTCACACATTTGAGTGGC	1020
Qy	1118	TATCACTTCAAACTGAAATTTGACCCAGACTCTTTTCAACAACTTCCAGTACCA	1177
Db	1021	TATCACTTCAAACTGAAATTTGACCCAGACTCTTTTCAACAACTTCCAGTACCA	1080
Qy	1178	AATCGTATTTGCTGTAATTTAACAACCTCTATCACTGAGCATCCCTCTGCTGACACC	1237
Db	1081	AATCGTATTTGCTGTAATTTAACAACCTCTATCACTGAGCATCCCTCTGCTGACACC	1140
Qy	1238	TTTCAATTCATGACACAAAAATCAACATATCAACAGTTTATCTACACAACTTATATTTG	1297
Db	1141	TTTCAATTCATGACACAAAAATCAACATATCAACAGTTTATCTACACAACTTATATTTG	1260
Qy	1298	CTGGAACATGGAATTAACCACTTTGTGATCATTTCAACAGCAAAATGCTGGAGGGTT	1357
Db	1201	CTGGAACATGGAATTAACCACTTTGTGATCATTTCAACAGCAAAATGCTGGAGGGTT	1260
Qy	1358	GCTGTGGTGAAGATTTTCCACCCGACGTACAGAAAAGTATCAACAGCTTCCATTGACAG	1417
Db	1261	GCTGTGGTGAAGATTTTCCACCCGACGTACAGAAAAGTATCAACAGCTTCCATTGACAG	1320
Qy	1418	AGCAGGAGATGAATAATACAGCTTTTAAAGTACCGCAAAAGCTTTATGCTGAAGCCC	1477
Db	1321	AGCAGGAGATGAATAATACAGCTTTTAAAGTATGATGATACGCAAAAGCTTTATGCTGAAGCCC	1380
Qy	1478	TATGATCATTTGAAGAACTTACAGAGAAAAAGAAATGTCGACAGATTGGAAGCACTC	1537
Db	1381	TATGATCATTTGAAGAACTTACAGAGAAAAAGAAATGTCGACAGATTGGAAGCACTC	1440
Qy	1538	TATGGTGACATGAGTGTGTGAGAGCTGTATCTGCTCTTCTGATGAAGAAAGCTCGGCCA	1597
Db	1441	TATGGTGACATGAGTGTGTGAGAGCTGTATCTGCTCTTCTGATGAAGAAAGCTCGGCCA	1500
Qy	1598	GATGCGATCTTTGGTGAAGAACCTGATGAAGTTGGAAGCACTCTCTTGAAGAGACTT	1657
Db	1501	GATGCGATCTTTGGTGAAGAACCTGATGAAGTTGGAAGCACTCTCTTGAAGAGACTT	1560
Qy	1658	ATGGGTAAATGTTATATGTTCTCTGCTCTACTGGAAGCAAGCACTTTTGGTGAAGAGT	1717
Db	1561	ATGGGTAAATGTTATATGTTCTCTGCTCTACTGGAAGCAAGCACTTTTGGTGAAGAGT	1620
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Qy	1838	GCAAGTCTTCCGCTCGAGCTAGATGATATCAATCCACAGTACTTAAAGAAAGCG	1897
Db	1741	GCAAGTCTTCCGCTCGAGCTAGATGATATCAATCCACAGTACTTAAAGAAAGCG	1800

Db	1741	GCAAGTCTTCCGCTCGAGCTAGATGATATCAATCCACAGTACTTAAAGAAAGCG	1800
Qy	1898	TCGACTGAACCTGTAG	1912
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RESULT 14

AR055229

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches 1814; Conservative

53.2%; Score 1803.2; DB 6; Length 1834;

99.0%; Pred. No. 0;

0; Mismatches 18; Indels 0; Gaps 0;

Qy	90	CCGCTGGAGTCTCGGCGCGGCTGCTGTCGCGCGGCTTGGGCTTCAAGCATACAG	149
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Qy	150	CAATCCCTTCTGTTCCCAACCATATGCAAAACCGAGTATATGATGATGAGATTTG	209
Db	61	CAATCCCTTCTGTTCCCAACCATATGCAAAACCGAGTATATGATGATGAGATTTG	120
Qy	210	ACGAGTATAGTCCGATTTGATCCCGGACAGATTTCTATGAGAGAAACCTGTCACACGG	269
Db	121	ACGAGTATAGTCCGATTTGATCCCGGACAGATTTCTATGAGAGAAACCTGTCACACGG	180
Qy	270	AATTTTGAAGAAATTAATTTCTGAACCCCACTCCAAACACAGTCACTATACATAC	329
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Qy	330	TTAACCACTTCAAGGATTTTGAACGTTGTGAATACATTCCTTCTTGAATGCA	389
Db	241	TTAACCACTTCAAGGATTTTGAACGTTGTGAATACATTCCTTCTTGAATGCA	300
Qy	390	TATAGTATGATGTTGACATCCAGATCACTTATGATGACATGTCACCACTTCAATG	449
Db	301	TATAGTATGATGTTGACATCCAGATCACTTATGATGACATGTCACCACTTCAATG	360
Qy	450	CTGACTATGCTTCAAAAGCTGGGAAGCTTCTTAACCTCTCTTAATTAACAGAGCC	509
Db	361	CTGACTATGCTTCAAAAGCTGGGAAGCTTCTTAACCTCTCTTAATTAACAGAGCC	420
Qy	510	TTCTCTCTGCTGATGATGTTGCGGACCTCCCTTGGGTGCAAAAGTAAAAAGAGCTTC	569
Db	421	TTCTCTCTGCTGATGATGTTGCGGACCTCCCTTGGGTGCAAAAGTAAAAAGAGCTTC	480
Qy	570	CTGATTCGAATGAGATTTGGAATAATTTCTTAAAGAAAGTTCATCCCTGATCCC	629
Db	481	CTGATTCGAATGAGATTTGGAATAATTTCTTAAAGAAAGTTCATCCCTGATCCC	540
Qy	630	AGGGCTCAAAACATGATGTTGATCTTTGCCAGACATTCACGACAGATTTTCAAGA	689
Db	541	AGGGCTCAAAACATGATGTTGATCTTTGCCAGACATTCACGATAGTTTTTCAAGA	600
Qy	690	CAGATCATTAAGGAGGCGAGCTTCAACCAAGGGCTGGGCGATGGGTGAGCTTAATC	749

Db 601 CAGATCAATTAACGCGGCGACCTTTCACCAAGCGGCTGGCCATGGGTGACCTTAATTC 660  
 Qy 750 ATATTACGCTGAAGCTCTGGCTAGACAGCGCTAAACCTGGCTTTTCAAGGATGAAAAA 809  
 Db 661 ATATTACGCTGAAGCTCTGGCTAGACAGCGCTAAACCTGGCTTTTCAAGGATGAAAAA 720  
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 Qy 870 AGATGATTAACCTCTCCAGAGCTCTGAGCAATCAAGCTTCTGGGAGAGAGCTCT 929  
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 Db 1261 GAGAGGTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
 Qy 1410 TTGACCAAGAGAGGAGATGAAATACAGTCTTTTATGATGATGATGATGATGATG 1469  
 Db 1321 TTGACCAAGAGAGGAGATGAAATACAGTCTTTTATGATGATGATGATGATGATG 1380  
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 Db 1381 TGAAGCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
 Qy 1530 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1589  
 Db 1441 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500  
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 Db 1501 CTGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
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 Db 1561 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
 Qy 1710 GAGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1769  
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 VERSION AR055235.1 GI:5980812  
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 ORGANISM  
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 REFERENCE  
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 AUTHORS Young, D.A., O'Banion, M.K. and Winn, V.D.  
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 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1814; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
 Qy 90 CCGCTGCGATGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 149  
 Db 1 CCGCTGCGATGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60  
 Qy 150 CAAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 209  
 Db 61 CAAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 Qy 210 ACCAGTATAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 269  
 Db 121 ACCAGTATAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
 Qy 270 AATTTTGAAGAATTAATTAATTTTGAAGAACCACTTCAACACAGTCACTATATG 329  
 Db 181 AATTTTGAAGAATTAATTAATTTTGAAGAACCACTTCAACACAGTCACTATATG 240  
 Qy 330 TTACCACTTCAAGGATTTTGAAGTGTGAATTAATTAATTAATTTTGAAGTGTGA 389  
 Db 241 TTACCACTTCAAGGATTTTGAAGTGTGAATTAATTAATTAATTTTGAAGTGTGA 300  
 Qy 390 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 449  
 Db 301 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 Qy 450 CTGACTATGCTTCAAAAGCTGGAAGCTTCTCTAACTTCTCTCTTATTAATGAGAGCC 509  
 Db 361 CTGACTATGCTTCAAAAGCTGGAAGCTTCTCTAACTTCTCTCTTATTAATGAGAGCC 420  
 Qy 510 TTCTCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 569  
 Db 421 TTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 Qy 570 CTGATTCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 629  
 Db 481 CTGATTCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
 Qy 630 AAGGCTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 689

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Db      541 AGGGCTCAACATGATGTTTGCAATCTTTGGCCAGACTTCAGCGCATTCAGTTTTCAGAA 600
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Db      601 CAGATCAATAAGCGAGGCCAGCTTTTACCCAAACGGGCTGGGCCCATGGGGTGAATTAAATC 660
QY      750 AATTTTACGGGTAACTCTGGCTAGACAGCGTAAATCTGGCCCTTTTTCAGAGATGAGAAAA 809
Db      661 AATTTTACGGGTAACTCTGGCTAGACAGCGTAAATCTGGCCCTTTTTCAGAGATGAGAAAA 720
QY      810 TGAATATATAGATTAATGATGAGAGATATATCTTCCCACTCAAGATCTCAGGCG 869
Db      721 TGAATATATAGATTAATGATGAGAGATATATCTTCCCACTCAAGATCTCAGGCG 780
QY      870 AGATGATCTACCCCTCTCAAGTCCCTGAGCATCTACGGTTTCTGGGGGCGAGGAGTCT 929
Db      781 AGATGATCTACCCCTCTCAAGTCCCTGAGCATCTACGGTTTCTGGGGGCGAGGAGTCT 840
QY      930 TTGCTCTGGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
Db      841 TTGCTCTGGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY      990 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1049
Db      901 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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QY      1110 TGAAGTCTATCATCTTCAAACTGAAATTTGACCCGAACTAATTTCACAAACAAATTC 1169
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QY      1170 AGTACCAAAATCGATTTGCTGCTGATTTTAAACCCCTCTATCATCTGCGCATCCCTCTGCG 1229
Db      1081 AGTACCAAAATCGATTTGCTGCTGATTTTAAACCCCTCTATCATCTGCGCATCCCTCTGCG 1140
QY      1230 CTGACACCTTTCAAATTCATGACAGCAAAATACAACTATCAACAGTTTATCTTACAAACA 1289
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QY      1290 CTATTTTCTGGAACATGGAATTAACCGATTTGTTGAATCATTCACAGGCAAAATGCTG 1349
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QY      1350 GCAGGGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1409
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QY      1410 TTGACAGAGCAGCAGATGAAATACCAAGTCTTTTAAAGTACCGCAAAACGCTTTATGCG 1469
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QY      1470 TGAAGCCCTTGAATCTTTTGAAGACTTACAGGAGAAAAAGAAATGCTGCAAGTGG 1529
Db      1381 TGAAGCCCTTGAATCTTTTGAAGACTTACAGGAGAAAAAGAAATGCTGCAAGTGG 1440
QY      1530 AAGCATCTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1589
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QY      1590 CTCGGCCAGATGCGATCTTTTGTGAAACCATGATGAGAGTGGAGACCATTCCTCTTGA 1649
Db      1501 CTCGGCCAGATGCGATCTTTTGTGAAACCATGATGAGAGTGGAGACCATTCCTCTTGA 1560
QY      1650 AAGCATCTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1709
Db      1561 AAGCATCTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY      1710 GAGAGTGGGTTTTCAAATCATCAACCTGCTCAATTCAGTCTTCTCATCTGCAATTAACG 1769

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Db      1681 TGAAGGCTGTCCCTTTTACTTACTTCAAGTTCAGATCCAGAGCTCATTTAAACAGTCA 1740
QY      1830 CCATCAATGCAAGTCTTCCCGCTCGGACTGATGATGATGATGATGATGATGATGATGATGAT 1889
Db      1741 CCATCAATGCAAGTCTTCCCGCTCGGACTGATGATGATGATGATGATGATGATGATGATGAT 1800
QY      1890 AAGAACGCTGCACTGAACTGATGAACTGAAT 1921
Db      1801 AAGAACGCTGCACTGAACTGATGAACTGAAT 1832

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 Job time : 12776 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 07:21:42 ; Search time 1217 Seconds

(without alignments)  
11823.046 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387

Sequence: 1 GTCCAGCAACTCCTCAGCAG.....GATTAAAAAAAAAAAAA 3387

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseg19908:\*  
3: geneseg20006:\*  
4: geneseg2001as:\*  
5: geneseg2001bs:\*  
6: geneseg20028:\*  
7: geneseg2003as:\*  
8: geneseg2003bs:\*  
9: geneseg2003cs:\*  
10: geneseg2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3385.4	100.0	3387	2	AAQ89376 Human cyc
2	3380.6	99.8	3387	2	AAQ71002 Cyclooxygenase
3	3379.9	99.8	3387	3	AAA34993 Human ade
4	3379.9	99.8	3387	3	AAQ21115 Human low
5	3379.9	99.8	3387	6	ABR94344 Human cyc
6	3379.9	99.8	3387	7	ABR96809 Human cyc
7	3379.9	99.8	3387	7	ACF63365 Human cyc
8	3379.9	99.8	3387	7	AAA34995 Human ade
9	3379.9	99.8	3387	7	AAQ21117 Human low
10	3379.9	99.8	3387	7	ABR96811 Human nuc
11	3216.6	95.0	4465	6	ABR77992 Hypoxia-r
12	3216.6	95.0	4465	7	ABX08805 Angiogene
13	3216.6	95.0	4465	8	ACCS7774 Human cyc
14	3216.6	95.0	4465	7	ACF79931 Breast ca
15	3215.9	94.9	4496	7	ACQ03925 CDNA down
16	3215.9	94.9	4496	7	ABR63478 Human CDN
17	3215.9	94.9	4496	7	ABR25722 Human CDN
18	2513.4	74.2	2563	7	ABR63477 Human CDN
19	1819.2	53.7	1834	5	AAV59635 Human pro
20	1810.2	53.4	1815	5	AAV59635 Human pro
21	1787.2	52.8	1834	2	AAQ61790 Sequence
22	1727.8	51.0	9979	5	AAV59635 Human pro
23	1727	51.0	9451	6	ABR97450 Human cyc

24	1727	51.0	9453	3	AAQ21116	AAQ21116 Human low
25	1727	51.0	9453	6	ABR65014	ABR65014 Lung can
26	1727	51.0	9453	6	ABR84194	ABR84194 Human CDN
27	1727	51.0	9453	7	ABR26810	ABR26810 Human nuc
28	1725.4	50.9	9453	3	AAA34994	AAA34994 Human ade
29	1719	50.8	11064	8	ADA20274	ADA20274 Human cyc
30	1621.6	47.9	3509	6	ABR88554	ABR88554 DNA encod
31	1621.6	47.9	3509	6	ABR88554	ABR88554 Dog prost
32	1620	47.8	3632	6	ABR94342	ABR94342 Canine cy
33	1528.6	45.1	4152	6	ABR19869	ABR19869 Mouse isc
34	1525.8	45.0	3986	6	ACCS7776	ACCS7776 Mouse cyc
35	1476.6	43.6	1812	6	ABR88557	ABR88557 Dog prost
36	1476.6	43.6	1812	6	ABR88556	ABR88556 Dog prost
37	1431.8	42.3	4404	9	ADRS2828	ADRS2828 Primary r
38	1379.8	40.7	1920	2	AAV59634	AAV59634 Mouse pro
39	1378.8	40.7	1920	2	AAQ61791	AAQ61791 Sequence
40	805.4	23.8	882	3	AAA30866	AAA30866 Breast ca
41	728.6	21.5	1819	2	AAV59640	AAV59640 Human pro
42	727.6	21.5	1800	6	ABR41943	ABR41943 Nucleotid
43	727.6	21.5	1807	9	ADG24198	ADG24198 Human NOV
44	727.6	21.5	1894	9	ADD27927	ADD27927 Human hco
45	727.6	21.5	2554	6	ABR76502	ABR76502 CDNA enco

## ALIGNMENTS

RESULT 1	AAQ89376	standard; CDNA; 3387 BP.
XX	AAQ89376;	
AC	25-MAR-2003 (revised)	
DT	28-SEP-1995 (first entry)	
XX	Human cyclooxygenase-2 CDNA.	
XX	Cyclooxygenase-2; COX-2; COX-1, inhibitor; screening; osteosarcoma; ss.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	CDS	98..1912
FT		/*tag= a
XX	W09509238-A1.	
XX	06-APR-1995.	
XX	13-SEP-1994; 94MO-CA000501.	
XX	27-SEP-1993; 93US-00084033.	
XX	(MERI ) MERCK FROST CANADA INC.	
XX	Oneil GP, Mancini JA;	
XX	WPI; 1995-147436/19.	
XX	P-PSDB; AAR72228.	
XX	High level expression of human cyclooxygenase (COX)-2 - using new 3' flanking region from COX-1, useful in assays for identifying potent, selective or preferential inhibitors of COX-2.	
XX	Disclosure; Fig 2; 59pp; English.	
XX	Full-length CDNA derived from human osteosarcoma cells (given in	
XX	AAQ89376) encoded human COX-2 (AAR72228). High-level expression of COX-2	
XX	in COS7 cells was achieved using a vaccinia or baculovirus vector and a	
XX	construct in which COX-2 CDNA was attached at its 5' end to a 3' flanking	
XX	sequence of human COX-1 CDNA (AAQ89377). (Updated on 25-MAR-2003 to	
XX	correct PN field.)	

XX Sequence 3387 BP; 1010 A; 714 C; 632 G; 1031 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 3385.4; DB 2; Length 3387;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 421 TTGATTTGACAGTCCACCAATCTACATGCTGACTATGCTACAAAAGCTGGAAACCTT 480  
 QY 481 CTCTAACTCTCTCTCTATTAATCTAAGAGCCCTCTCTCTGCTGATGATTTGCCGACTCC 540  
 DB 481 CTCTAACTCTCTCTCTATTAATCTAAGAGCCCTCTCTCTGCTGATGATTTGCCGACTCC 540  
 QY 541 CTGCGGTGTCAAAAGTAAAGAGAGCTTCTCTGATTAAGATTAAGATTTGGAATTTGCT 600  
 DB 541 CTGCGGTGTCAAAAGTAAAGAGAGCTTCTCTGATTAAGATTAAGATTTGGAATTTGCT 600  
 QY 601 TCTPAAGAAAGATTCATCCCTGATCCCGCAGGCTCAAAACATGATGTTTGCATTTTGC 660  
 DB 601 TCTPAAGAAAGATTCATCCCTGATCCCGCAGGCTCAAAACATGATGTTTGCATTTTGC 660  
 QY 661 CCAGCACTTCAACGACCAAGTTTTCAGAGATCAATACGAGGCGGCGACCTTTCACCA 720  
 DB 661 CCAGCACTTCAACGACCAAGTTTTCAGAGATCAATACGAGGCGGCGACCTTTCACCA 720  
 QY 721 CGGCGTGTGCAATGAGGCTGACTTAATCATATTTCCGTTAACTCTGCTGACAGCG 780  
 DB 721 CGGCGTGTGCAATGAGGCTGACTTAATCATATTTCCGTTAACTCTGCTGACAGCG 780  
 QY 781 TAAACTGCGCTTTTCAGAGATGAGAAATGAAATATCAGATTAATGATGAGAGATGTA 840  
 DB 781 TAAACTGCGCTTTTCAGAGATGAGAAATGAAATATCAGATTAATGATGAGAGATGTA 840  
 QY 841 TCTCTCCACAGTCAAAAGATCTCAGGCAAGATGATCTACCTCTCAATCTCCTGAGCA 900  
 DB 841 TCTCTCCACAGTCAAAAGATCTCAGGCAAGATGATCTACCTCTCAATCTCCTGAGCA 900  
 QY 901 TCTAAGTGTGTGTGCGGAGAGAGCTTGTGCTGTGCTGTGCTGTGATGATGTC 960  
 DB 901 TCTAAGTGTGTGTGCGGAGAGAGCTTGTGCTGTGCTGTGCTGTGATGATGTC 960  
 QY 961 CACAATCTGCTGCGGAGACAAACAGAGTATGATGCTTAAACAGAGATCCTGTA 1020

DB 961 CACAATCTGCTGCGGAGACAAACAGAGTATGATGCTTAAACAGAGATCCTGTA 1020  
 QY 1021 ATGGGCTGATGACAGTGTGTCACAGCAAGCGCTAATACATGATGAGAGACATTTAA 1080  
 DB 1021 ATGGGCTGATGACAGTGTGTCACAGCAAGCGCTAATACATGATGAGAGACATTTAA 1080  
 QY 1081 GATTTGATGAGATTTATGTCGCAACCTGAGTGGCTATCACTTCAACTGAATTTGA 1140  
 DB 1081 GATTTGATGAGATTTATGTCGCAACCTGAGTGGCTATCACTTCAACTGAATTTGA 1140  
 QY 1141 CCCAGAACTACTTTTCAACAAATTCAGATCAACAAATGATATGCTGTGAATTTAA 1200  
 DB 1141 CCCAGAACTACTTTTCAACAAATTCAGATCAACAAATGATATGCTGTGAATTTAA 1200  
 QY 1201 CACCTCTATCTGTCATCTCCCTCTGCTGTGACACCTTTGAAATTCAGACAGAAAT 1260  
 DB 1201 CACCTCTATCTGTCATCTCCCTCTGCTGTGACACCTTTGAAATTCAGACAGAAAT 1260  
 QY 1261 CAACTATCAACAGTTATCTAACAACATCTAATTTGCTGGAACATGGAATTTACCA 1320  
 DB 1261 CAACTATCAACAGTTATCTAACAACATCTAATTTGCTGGAACATGGAATTTACCA 1320  
 QY 1321 TGTGATATCTTACCAAGCAATTTGCTGAGGCTGTGCTGTGATGAGAAATGTCAC 1380  
 DB 1321 TGTGATATCTTACCAAGCAATTTGCTGAGGCTGTGCTGTGATGAGAAATGTCAC 1380  
 QY 1381 CGCAGTACAGAAAGTATCAACAGCTTCCATTCACAGACAGACAGAGATGAATACAG 1440  
 DB 1381 CGCAGTACAGAAAGTATCAACAGCTTCCATTCACAGACAGACAGATGAATACAG 1440  
 QY 1441 TTTTAAATGATACCGCAACGCTTTATGCTGGAAGCCCTATGATCAATTTGAACCTT 1500  
 DB 1441 TTTTAAATGATACCGCAACGCTTTATGCTGGAAGCCCTATGATCAATTTGAACCTT 1500  
 QY 1501 ACGAGAAAGAAATGTCTGACAGATTGGAAGACCTTATGCTGATGATGCTGTGGA 1560  
 DB 1501 ACGAGAAAGAAATGTCTGACAGATTGGAAGACCTTATGCTGATGATGCTGTGGA 1560  
 QY 1561 GCTGTATCTGCTCTCTGTGTGAAGAGCTGCGGACAGATGCAATTTTGTGGAACAT 1620  
 DB 1561 GCTGTATCTGCTCTCTGTGTGAAGAGCTGCGGACAGATGCAATTTTGTGGAACAT 1620  
 QY 1621 GGTAGAGTTGAGACACATCTCTCTTGAAGAGCTTATGAGTATGTTATGTTCTCC 1680  
 DB 1621 GGTAGAGTTGAGACACATCTCTCTTGAAGAGCTTATGAGTATGTTATGTTCTCC 1680  
 QY 1681 TGCCTATCTGAAAGCCAGACATTTTGTGTGAGAGATGCGTTTCAATCATCAACTGC 1740  
 DB 1681 TGCCTATCTGAAAGCCAGACATTTTGTGTGAGAGATGCGTTTCAATCATCAACTGC 1740  
 QY 1741 CTCATTTAGTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTACTTCACTTCACTGT 1800  
 DB 1741 CTCATTTAGTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTACTTCACTTCACTGT 1800  
 QY 1801 TCCAGATCCAGAGCTCATTAATAACAGTCAACATCAATGCAAGTTCTCCGCTCCGAG 1860  
 DB 1801 TCCAGATCCAGAGCTCATTAATAACAGTCAACATCAATGCAAGTTCTCCGCTCCGAG 1860  
 QY 1861 AGATGATATCAATCCCAAGTACTACTTAAAGAGCGTGAAGTGAAGTGAAGTGA 1920  
 DB 1861 AGATGATATCAATCCCAAGTACTACTTAAAGAGCGTGAAGTGAAGTGAAGTGA 1920  
 QY 1921 TGAATCATTTATTTATTTATATGAACATGCTATTAATTAATTAATTAATTAATTT 1980  
 DB 1921 TGAATCATTTATTTATTTATATGAACATGCTATTAATTAATTAATTAATTAATTT 1980  
 QY 1981 ATATTAACCTCTTATGTTACTTAATCACTTCTGTAACAGAACTGATCTCTGTGCG 2040  
 DB 1981 ATATTAACCTCTTATGTTACTTAATCACTTCTGTAACAGAACTGATCTCTGTGCG 2040  
 QY 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGCTCACTCTTAAGATTTTGTGTTGC 2100  
 DB 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGCTCACTCTTAAGATTTTGTGTTGC 2100

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QY 2101 TGTAGTTTGGAAAAAGTTTATTTCTGTTTATTAACACAGAGAAATGAGTTTGA 2160
Db 2101 TGTAAAGTTTGGAAAAAGTTTATTTCTGTTTATTAACACAGAGAAATGAGTTTGA 2160
QY 2161 CGCTTTTAACTTGAATTTCACTTATTAATTAAGAGCAAGAAAGTATGTTGAATAC 2220
Db 2161 CGCTTTTAACTTGAATTTCACTTATTAATTAAGAGCAAGAAAGTATGTTGAATAC 2220
QY 2221 TTAACACATATACCAAGATGCCAAAATGCTGAAGTTTAACTGTGCATGTTTCCAT 2280
Db 2221 TTAACACATATACCAAGATGCCAAAATGCTGAAGTTTAACTGTGCATGTTTCCAT 2280
QY 2281 GGAATCTTCATGATGATTAAGAAATTAATGTTTGAATTTTAAAGTATCTTTGGGTA 2340
Db 2281 GGAATCTTCATGATGATTAAGAAATTAATGTTTGAATTTTAAAGTATCTTTGGGTA 2340
QY 2341 TTTTCTGTCATCAAAACAAAACAGGATATGAGCATATTAATTAATGAAATTTTGA 2400
Db 2341 TTTTCTGTCATCAAAACAAAACAGGATATGAGCATATTAATTAATGAAATTTTGA 2400
QY 2401 CATTAACAGTAATTTATGATGATCTTTTAAATAGCAATGAAACAAATATTTGAAAT 2460
Db 2401 CATTAACAGTAATTTATGATGATCTTTTAAATAGCAATGAAACAAATATTTGAAAT 2460
QY 2461 TCTAATTCATGAGGTAAGATACCTGTAAAGCTTTGTTGATTTCTTAAAGTTTAA 2520
Db 2461 TCTAATTCATGAGGTAAGATACCTGTAAAGCTTTGTTGATTTCTTAAAGTTTAA 2520
QY 2521 CTGTGACATATACCAAAAAAGAGCTGTGATTTAAATCTGTAAATCAGATCAAAAT 2580
Db 2521 CTGTGACATATACCAAAAAAGAGCTGTGATTTAAATCTGTAAATCAGATCAAAAT 2580
QY 2581 TTACTACAAATGCTTTGTTAAATATTTTAAATAGTATGCTTTTCAACCAAGATTA 2640
Db 2581 TTACTACAAATGCTTTGTTAAATATTTTAAATAGTATGCTTTTCAACCAAGATTA 2640
QY 2641 AACCTTTTATGATGATGCTTTAAACCTTCTTTTAAATCAAAATGCCAAATTTTAAAG 2700
Db 2641 AACCTTTTATGATGATGCTTTAAACCTTCTTTTAAATCAAAATGCCAAATTTTAAAG 2700
QY 2701 TGTGAGAGCCACTGAGTATATCTCAAAATTAAGAAATCTCTGTGAGATATTCAGAT 2760
Db 2701 TGTGAGAGCCACTGAGTATATCTCAAAATTAAGAAATCTCTGTGAGATATTCAGAT 2760
QY 2761 CTGTTTATATGCTGTGTAACATGTAAAAACCCCATTAACCCGCCAAAAGGGGTCTTACC 2820
Db 2761 CTGTTTATATGCTGTGTAACATGTAAAAACCCCATTAACCCGCCAAAAGGGGTCTTACC 2820
QY 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTGCCAAATTTAGGGT 2880
Db 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGTTGCCAAATTTAGGGT 2880
QY 2881 TTAACCTTTTGAAGCAAACTTTTAAAGCTGTGACAGCGAGACTGTACTCAGAT 2940
Db 2881 TTAACCTTTTGAAGCAAACTTTTAAAGCTGTGACAGCGAGACTGTACTCAGAT 2940
QY 2941 TTTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTAATTAACATATGTTTCTCAGAT 3000
Db 2941 TTTGCTATGAGGTTAATGAAGTACCAAGCTGTGCTTAATTAACATATGTTTCTCAGAT 3000
QY 3001 TTTTCTGTTTACAGTTTAAATTTAGCAGTCCATATCAGATTGCAAAAGTAGACATC 3060
Db 3001 TTTTCTGTTTACAGTTTAAATTTAGCAGTCCATATCAGATTGCAAAAGTAGACATC 3060
QY 3061 ATAAATTAACCTCTCAAAATGCTTAATTAATTAATTAATTAATTTTATCTAGCTTG 3120
Db 3061 ATAAATTAACCTCTCAAAATGCTTAATTAATTAATTAATTAATTTTATCTAGCTTG 3120
QY 3121 AAGCAATTCAGTAGTGAATGCAATCAAGCTGTGCTAGCTGATCTGTCTTCTTCT 3180
Db 3121 AAGCAATTCAGTAGTGAATGCAATCAAGCTGTGCTAGCTGATCTGTCTTCTTCT 3180

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QY 3181 TTTCTCTTTTAGCCATTTTGTGTAAGACACAGCTCTTCAAAACATTCGTTTCTCTA 3240
Db 3181 TTTCTCTTTTAGCCATTTTGTGTAAGACACAGCTCTTCAAAACATTCGTTTCTCTA 3240
QY 3241 TTTTGTTTTACTAGTTTAAAGATCAGAGTTCATCTTCTTGAACCTGACCTATTTCT 3300
Db 3241 TTTTGTTTTACTAGTTTAAAGATCAGAGTTCATCTTCTTGAACCTGACCTATTTCT 3300
QY 3301 TACCTGAACCTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGAGCTGATTTAGTCTC 3360
Db 3301 TACCTGAACCTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGAGCTGATTTAGTCTC 3360
QY 3361 TTAAGAGATTAATAAAAAAAAAAG 3387
Db 3361 TTAAGAGATTAATAAAAAAAAAAG 3387

RESULT 2
AAQ71002
ID AAQ71002 standard; cDNA; 3387 BP.
XX
AC AAQ71002;
XX
AC 25-MAR-2003 (revised)
DT 27-FEB-1995 (first entry)
XX
DE Cyclooxygenase-2 cDNA.
XX
KM Cyclooxygenase-2; enzyme; osteosarcoma; assay; ss.
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT CDS 57..1910
FT /tag= a
FT /label= cyclooxygenase-2

W09414977-A1.
XX
PD 07-JUL-1994.
XX
PF 17-DEC-1993; 93WO-CA000547.
XX
PR 22-DEC-1992; 92US-00994760.
PR 06-MAY-1993; 93US-00064271.
XX
PA (MERI ) MERCK FROST CANADA INC.
XX
PI Cromlish WA, Kennedy BP, Oneill G, Vickers PJ, Wong E;
PI Mancini JA;
XX
DR WPI; 1994-263635/32.
DR P-PSDB; AAR56660.
XX
PT Assays for cyclo-oxygenase-1 and -2 - for identifying selective
PT antagonists, i.e. potential anti-inflammatory etc., also new human
PT cyclo-oxygenase-2 and cDNA encoding it.
XX
PS Disclosure; Fig 2A-2C; 55pp; English.
XX
CC The human cyclooxygenase-2 cDNA is isolated from osteosarcoma cells, and
CC is expressed from a mammalian or eukaryotic vector. The COX-2 protein is
CC used in assays to identify inhibitors which have anti-inflammatory,
CC antipyretic, analgesic and anticancer activity. (Updated on 25-MAR-2003
CC to correct FN field.)
XX
SQ Sequence 3387 BP; 1010 A; 715 C; 631 G; 1031 T; 0 U; 0 Other;

Query Match 99.8%; Score 3380.6; DB 2; Length 3387;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3383; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCAGGAACCTCTCAGACAGCGCTCTTCACTCCACAGCCGAGCGCCTCAGACGCA 60

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QY 2221 TTAAACGCTATCAAGATGCCAAATGCTGAAAGTTTTCACCTGTCAGTGTTCAT 2280  
 DB 2221 TTAAACGCTATCAAGATGCCAAATGCTGAAAGTTTTCACCTGTCAGTGTTCAT 2280  
 QY 2281 GCATCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
 DB 2281 GCATCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
 QY 2341 TTTTCTGTCATCAAAACAAACAGATATGATGATGATGATGATGATGATGATGATGAT 2400  
 DB 2341 TTTTCTGTCATCAAAACAAACAGATATGATGATGATGATGATGATGATGATGATGAT 2400  
 QY 2401 CATTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
 DB 2401 CATTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
 QY 2461 TCTAAATTCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 DB 2461 TCTAAATTCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 QY 2521 CTTGATACATATACCAAAAGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 2580  
 DB 2521 CTTGATACATATACCAAAAGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 2580  
 QY 2581 TTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
 DB 2581 TTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
 QY 2641 AACCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700  
 DB 2641 AACCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700  
 QY 2701 TGGTGGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 DB 2701 TGGTGGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 QY 2761 CTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
 DB 2761 CTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
 QY 2821 TTGAACATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTA 2880  
 DB 2821 TTGAACATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTA 2880  
 QY 2881 TTAAACCTTTTGAAGCAACTTTTGAAGCAACTTTTGAAGCAACTTTTGAAGCAACTTTT 2940  
 DB 2881 TTAAACCTTTTGAAGCAACTTTTGAAGCAACTTTTGAAGCAACTTTTGAAGCAACTTTT 2940  
 QY 2941 TTTGCTATGAGGATTAAGCAAGTACCAAGCTGCTGATTAAGCAAGTATGTTTTCAGAT 3000  
 DB 2941 TTTGCTATGAGGATTAAGCAAGTACCAAGCTGCTGATTAAGCAAGTATGTTTTCAGAT 3000  
 QY 3001 TTTGCTGATGAGGATTAAGCAAGTACCAAGCTGCTGATTAAGCAAGTATGTTTTCAGAT 3060  
 DB 3001 TTTGCTGATGAGGATTAAGCAAGTACCAAGCTGCTGATTAAGCAAGTATGTTTTCAGAT 3060  
 QY 3061 ATAAATATCTCTTCAAAATGCTTAATATCAACATTAATTAATCAACATTAATTAATCAAC 3120  
 DB 3061 ATAAATATCTCTTCAAAATGCTTAATATCAACATTAATTAATCAACATTAATTAATCAAC 3120  
 QY 3121 AAGCCAAATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 DB 3121 AAGCCAAATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 QY 3181 TTTTCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
 DB 3181 TTTTCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
 QY 3241 TTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
 DB 3241 TTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300

QY 3301 TACCTGACCTTTTGAAGGATTTTTCAGGATTAACCTCAGCTCAGTCTATTAAGTCTC 3360  
 DB 3301 TACCTGACCTTTTGAAGGATTTTTCAGGATTAACCTCAGCTCAGTCTATTAAGTCTC 3360  
 QY 3361 TTAAAGAGATTTAAAAAAG 3387  
 DB 3361 TTAAAGAGATTTAAAAAAG 3387  
 RESULT 3  
 AAA34993  
 ID AAA34993 standard; DNA; 3387 BP.  
 XX  
 AC AAA34993;  
 XX  
 DT 28-UTL-2000 (first entry)  
 XX  
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2682.  
 DE  
 XX Human: adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;  
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US017712.  
 XX  
 PR 03-AUG-1998; 98US-0095212P.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JM;  
 XX  
 PS WPI; 2000-205971/18.  
 DR  
 XX  
 PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 XX Disclosure; Page 890-891; 1343pp; English.  
 PS  
 XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cyostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.

CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO. sequences given in the sequence  
listing

XX Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 3; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 GTCCAGAACTCTTCAAGAGGCTCTTCACTCAGCCAGCCAGAGCCCTCAGACAGA 60
DB 1 GTCCAGAACTCTCAGAGGCTCTTCACTCAGCCAGCCAGAGCCCTCAGACAGA 60
QY 61 AAGCTTACCCCGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGT 120
DB 61 AAGCTTACCCCGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGT 120
QY 121 GTGCGGCTCTGCGCGCTCAGCCATACAGCAATCTTGTCTGCTCCACCAATGTCAAA 180
DB 121 GTGCGGCTCTGCGCGCTCAGCCATACAGCAATCTTGTCTGCTCCACCAATGTCAAA 180
QY 181 CGAGAGTATATATATATATATATATATATATATATATATATATATATATATAT 240
DB 181 CGAGAGTATATATATATATATATATATATATATATATATATATATATATATAT 240
QY 241 ATTCTATGAGAAATATGTCACACCGGAAATTTTGAAGAATTAATTTCTGAA 300
DB 241 ATTCTATGAGAAATATGTCACACCGGAAATTTTGAAGAATTAATTTCTGAA 300
QY 301 ACCCACTCCAAACAGTGCATACATACCTTCAAGGAGTTTGGAACTGTGT 360
DB 301 ACCCACTCCAAACAGTGCATACATACCTTCAAGGAGTTTGGAACTGTGT 360
QY 361 GAATAACATTCCTCTCTTGGAAATGCAATATATATATATATATATATATATAT 420
DB 361 GAATAACATTCCTCTCTTGGAAATGCAATATATATATATATATATATATATAT 420
QY 421 TTGTATGAGAGTCCCAACTTACATGCTGCTATGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TTGTATGAGAGTCCCAACTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CTCTAACCTCTCTATATATATAGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCT 540
DB 481 CTCTAACCTCTCTATATATATAGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCT 540
QY 541 CTGAGTGTCAAAAGTAAAGAGAGCTCTCTGATTCAAATGAGATTTGGAAATTTGCT 600
DB 541 CTGAGTGTCAAAAGTAAAGAGAGCTCTCTGATTCAAATGAGATTTGGAAATTTGCT 600
QY 601 TCTTAAGAGAAATGATCCCTGATCCCAAGGCTCAAAAGATGATTTGCTTCTTGC 660
DB 601 TCTTAAGAGAAATGATCCCTGATCCCAAGGCTCAAAAGATGATTTGCTTCTTGC 660
QY 661 CCAGCACTTCAGCATCAGTTTTCAGAGACATTAAGCGAGGCGAGCTTTCACAA 720
DB 661 CCAGCACTTCAGCATCAGTTTTCAGAGACATTAAGCGAGGCGAGCTTTCACAA 720
QY 721 CGGAGCTGGGCGATGGGCTGATTAATATATATATATATATATATATATATAT 780
DB 721 CGGAGCTGGGCGATGGGCTGATTAATATATATATATATATATATATATATAT 780
QY 781 TAAAGCGGCTTTTCAAGAGTGAATAATGAAATATCAGATTAATGATGAGATGTA 840
DB 781 TAAAGCGGCTTTTCAAGAGTGAATAATGAAATATCAGATTAATGATGAGATGTA 840
QY 841 TCTCTCCACAGTCAAAAGATCTCAGGCAAGATGATCTACCTCTCAAGTCTCTGAGCA 900
DB 841 TCTCTCCACAGTCAAAAGATCTCAGGCAAGATGATCTACCTCTCAAGTCTCTGAGCA 900
QY 901 TCTACGTTTGTCTGTGGGCGAGAGGCTTTGTGCTGTGGCTGTGTGTATGTATGC 960
DB 901 TCTACGTTTGTCTGTGGGCGAGAGGCTTTGTGCTGTGGCTGTGTGTATGTATGC 960
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QY 961 CACAACTCTGGCTGGGGAACAAACAGATATGATGCTTAAACAGAGACTCTGA 1020
DB 961 CACAACTCTGGCTGGGGAACAAACAGATATGCAATGTGCTTAAACAGAGACTCTGA 1020
QY 1021 ATGGGCTATGAGCAGTTTCTTCCAGACAGAGCTTAATCTGATGAGAGACTATTA 1080
DB 1021 ATGGGCTATGAGCAGTTTCTTCCAGACAGAGCTTAATCTGATGAGAGACTATTA 1080
QY 1081 GATTGTGATGAAATTTATGAGCACTTGAATGGCTATACCTTCAAACTGAAATTTGA 1140
DB 1081 GATTGTGATGAAATTTATGAGCACTTGAATGGCTATACCTTCAAACTGAAATTTGA 1140
QY 1141 CCCAGAACTACTTTCAACAAACATTCAGTCCAAATGCTATGCTGTAATTTAA 1200
DB 1141 CCCAGAACTACTTTCAACAAACATTCAGTCCAAATGCTATGCTGTAATTTAA 1200
QY 1201 CACCTCTATCACTGGCATCCCTCTCTGCTGACACTTTCAAATTCATGACCAAAAT 1260
DB 1201 CACCTCTATCACTGGCATCCCTCTCTGCTGACACTTTCAAATTCATGACCAAAAT 1260
QY 1261 CAAGTATCAAGTATATCAACAGACTATATATGCTGGAACATGGAATACCAAT 1320
DB 1261 CAAGTATCAAGTATATCAACAGACTATATATGCTGGAACATGGAATACCAAT 1320
QY 1321 TGTGATCATTCACAGGCAATTTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TGTGATCATTCACAGGCAATTTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CGCAGTACAGAAATATCAAGGCTTCCATATGACCAAGCAGGAGATGAATACCAAT 1440
DB 1381 CGCAGTACAGAAATATCAAGGCTTCCATATGACCAAGCAGGAGATGAATACCAAT 1440
QY 1441 TTTTATGAGTACCGGAAACGCTTATGCTGAAGCCCTATGATCAATTTGAAGAACTTAC 1500
DB 1441 TTTTATGAGTACCGGAAACGCTTATGCTGAAGCCCTATGATCAATTTGAAGAACTTAC 1500
QY 1501 AGAGAGAAAGAAATGTCTGAGAGTGGAGCACTATATGCTGATCATGATGCTGTGA 1560
DB 1501 AGAGAGAAAGAAATGTCTGAGAGTGGAGCACTATATGCTGATCATGATGCTGTGA 1560
QY 1561 GCTGTATCTGCTGCTTCTGCTGAGAAAGCTTGGCGAGATGCTGCTGCTGCTGCT 1620
DB 1561 GCTGTATCTGCTGCTTCTGCTGAGAAAGCTTGGCGAGATGCTGCTGCTGCTGCT 1620
QY 1621 GGTAGAGTTGAGAGCACTTCTCTTGAAGAACTTATGAGGTAATGTTATGTTCTCC 1680
DB 1621 GGTAGAGTTGAGAGCACTTCTCTTGAAGAACTTATGAGGTAATGTTATGTTCTCC 1680
QY 1681 TGCTTACCTGGAAGCCAGCACTTTTGTGAGAAAGTGGGTTTCAATCATCAACACTGC 1740
DB 1681 TGCTTACCTGGAAGCCAGCACTTTTGTGAGAAAGTGGGTTTCAATCATCAACACTGC 1740
QY 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCTTACTTCACTGAGTGT 1800
DB 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCTTACTTCACTGAGTGT 1800
QY 1801 TCCAGATCCAGAGCTCATTAACAGTCAACATCAATGCAAGTCTTCCGCTCGGAGCT 1860
DB 1801 TCCAGATCCAGAGCTCATTAACAGTCAACATCAATGCAAGTCTTCCGCTCGGAGCT 1860
QY 1861 AGATGATATCAATCCCAAGTACTTCAAAAGAGAGCTGCAAGAGCTGAGAGCTTAA 1920
DB 1861 AGATGATATCAATCCCAAGTACTTCAAAAGAGAGCTGCAAGAGCTGAGAGCTTAA 1920
QY 1921 TGAATATATATATATATATATATATATATATATATATATATATATATATATAT 1980
DB 1921 TGAATATATATATATATATATATATATATATATATATATATATATATATATAT 1980
QY 1981 ATATTAACCTCTTATATATATATATATATATATATATATATATATATATATATAT 2040
DB 1981 ATATTAACCTCTTATATATATATATATATATATATATATATATATATATATATAT 2040
```

QY 2041 GAGAAAGAGTCACTGAGAGACTTTTANGTCACTACTTAAGATTTCCTGCTGC 2100  
 Db 2041 GAGAAAGAGTCACTGAGAGACTTTTANGTCACTACTTAAGATTTCCTGCTGC 2100  
 QY 2101 TGTAAAGTTGAAAAAGTTTATCTGTTTATTAACCAAGAGAAATGCTTTGA 2160  
 Db 2101 TGTAAAGTTGAAAAAGTTTATCTGTTTATTAACCAAGAGAAATGCTTTGA 2160  
 QY 2161 CGCTTTTACTGAAATTTCACTTAATTAAGAGCAAGAAAGTGTGAATAC 2220  
 Db 2161 CGCTTTTACTGAAATTTCACTTAATTAAGAGCAAGAAAGTGTGAATAC 2220  
 QY 2221 TTAACACTATCAAGAGAGCCAAATGCTGAAGTTTTCACCTGCAATGTTTCAAT 2280  
 Db 2221 TTAACACTATCAAGAGAGCCAAATGCTGAAGTTTTCACCTGCAATGTTTCAAT 2280  
 QY 2281 GCATCTTCATGATGATTAAGAAATGCTTAATGTTGAATTTTAAAGTCTTTGGGA 2340  
 Db 2281 GCATCTTCATGATGATTAAGAAATGCTTAATGTTGAATTTTAAAGTCTTTGGGA 2340  
 QY 2341 TTTTCTGTCATCAAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
 Db 2341 TTTTCTGTCATCAAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
 QY 2401 CATTAACAGTATTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
 Db 2401 CATTAACAGTATTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
 QY 2461 TCTAAATTCATGAGGTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 Db 2461 TCTAAATTCATGAGGTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 QY 2521 CTGTAACATATACCAAAAGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 2580  
 Db 2521 CTGTAACATATACCAAAAGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 2580  
 QY 2581 TTACAGCAATGCTGTTTAAATTTTATTAAGATGATGATGATGATGATGATGATGATGAT 2640  
 Db 2581 TTACAGCAATGCTGTTTAAATTTTATTAAGATGATGATGATGATGATGATGATGATGAT 2640  
 QY 2641 AACCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700  
 Db 2641 AACCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700  
 QY 2701 TGTGAGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 Db 2701 TGTGAGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 QY 2761 CTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
 Db 2761 CTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
 QY 2821 TTGAACATTAAGCAATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
 Db 2821 TTGAACATTAAGCAATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
 QY 2881 TTAACCTTTTGAAGCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
 Db 2881 TTAACCTTTTGAAGCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
 QY 2941 TTTGCTATGAGGTATTAAGAGTACCAAGCTGCTGATGATGATGATGATGATGATGATGAT 3000  
 Db 2941 TTTGCTATGAGGTATTAAGAGTACCAAGCTGCTGATGATGATGATGATGATGATGATGAT 3000  
 QY 3001 TTTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
 Db 3001 TTTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
 QY 3061 ATAAATTAAGCTCTTCAAAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3120  
 Db 3061 ATAAATTAAGCTCTTCAAAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3120  
 QY 3121 AAGCAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180

Db 3121 AAGCAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 QY 3181 TTTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
 Db 3181 TTTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240  
 QY 3241 TTTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
 Db 3241 TTTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300  
 QY 3301 TACTGAATTTTGAAGTTTCAAGTAAACCTGAGCTGAGAGCTGATTTAGTCTGCTC 3360  
 Db 3301 TACTGAATTTTGAAGTTTCAAGTAAACCTGAGCTGAGAGCTGATTTAGTCTGCTC 3360  
 QY 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387  
 Db 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387

## RESULT 4

AAE21115 ID AAE21115 standard; DNA; 3387 BP.

AAE21115; 14-MAR-2001 (first entry)

Human low adenosine antisense oligonucleotide related sequence #2682.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 human; airway disorder; bronchoconstriction; lung inflammation;  
 surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;  
 respiratory obstruction; pulmonary obstruction; impeded respiration;  
 surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 cancer; se.

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020.

06-APR-1999; 99US-0127958P.

(UYEC-) UNIV EAST CAROLINA.

(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 965-966; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cyostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors,



CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impaired respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF1434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 CC  
 XX

SQ Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 3; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCAGGAATCTCTCAGACAGGCGCTCTTCAGCTCCACAGCCAGCGCTTACAGACAGA 60  
 Db 1 GTCCAGGAATCTCTCAGACAGGCGCTCTTCAGCTCCACAGCCAGCGCTTACAGACAGA 60  
 QY 61 AAGCTTACCCCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCT 120  
 Db 61 AAGCTTACCCCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCT 120  
 QY 121 GGGCGGCGCTCTGCGCGCTCAGCCATACAGCAAACTCTGCTGTCCACCCATGTCAAAA 180  
 Db 121 GGGCGGCGCTCTGCGCGCTCAGCCATACAGCAAACTCTGCTGTCCACCCATGTCAAAA 180  
 QY 121 GGGCGGCGCTCTGCGCGCTCAGCCATACAGCAAACTCTGCTGTCCACCCATGTCAAAA 180  
 Db 121 GGGCGGCGCTCTGCGCGCTCAGCCATACAGCAAACTCTGCTGTCCACCCATGTCAAAA 180  
 QY 181 CCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 Db 181 CCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 QY 241 ATTCTATGAGAAATGCTGCTCAACCGGATTTTGAACAAGATTAATTTATTTGAA 300  
 Db 241 ATTCTATGAGAAATGCTGCTCAACCGGATTTTGAACAAGATTAATTTATTTGAA 300  
 QY 241 ATTCTATGAGAAATGCTGCTCAACCGGATTTTGAACAAGATTAATTTATTTGAA 300  
 Db 241 ATTCTATGAGAAATGCTGCTCAACCGGATTTTGAACAAGATTAATTTATTTGAA 300  
 QY 301 ACCCATCCCAACACAGTGAATACATACCTTCAAGGATTTTGAACGTTGT 360  
 Db 301 ACCCATCCCAACACAGTGAATACATACCTTCAAGGATTTTGAACGTTGT 360  
 QY 301 ACCCATCCCAACACAGTGAATACATACCTTCAAGGATTTTGAACGTTGT 360  
 Db 301 ACCCATCCCAACACAGTGAATACATACCTTCAAGGATTTTGAACGTTGT 360  
 QY 361 GAATAACATTCCTCTCTGGAATGCAATTAATGATGATGATGATGATGATGATGATGATGAT 420  
 Db 361 GAATAACATTCCTCTCTGGAATGCAATTAATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 421 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 Db 421 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 QY 421 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 Db 421 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 QY 481 CTCTAACCTCTCTATTAATCTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
 Db 481 CTCTAACCTCTCTATTAATCTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
 QY 541 CTCTAACCTCTCTATTAATCTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 Db 541 CTCTAACCTCTCTATTAATCTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 QY 541 CTCTAACCTCTCTATTAATCTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 Db 541 CTCTAACCTCTCTATTAATCTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
 QY 601 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 Db 601 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 QY 601 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 Db 601 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 QY 661 CCAGCACTTACGACGACGATTTTCAAGACAGATCATTAAGCGAGGCGCTTCAACCA 720  
 Db 661 CCAGCACTTACGACGACGATTTTCAAGACAGATCATTAAGCGAGGCGCTTCAACCA 720

Db 661 CCAGCACTTACGACGACGATTTTCAAGACAGATCATTAAGCGAGGCGCTTCAACCA 720  
 QY 721 CCGGCTGGGCGCATGGGGTGGATTAATTCATTTAGGTGAATCTGCTGCTAGACAGC 780  
 Db 721 CCGGCTGGGCGCATGGGGTGGATTAATTCATTTAGGTGAATCTGCTGCTAGACAGC 780  
 QY 721 CCGGCTGGGCGCATGGGGTGGATTAATTCATTTAGGTGAATCTGCTGCTAGACAGC 780  
 Db 721 CCGGCTGGGCGCATGGGGTGGATTAATTCATTTAGGTGAATCTGCTGCTAGACAGC 780  
 QY 781 TAACTGGGCTTTTCAAGATGAGAAATATCAATTAATGATGATGATGATGATGATGATGATGAT 840  
 Db 781 TAACTGGGCTTTTCAAGATGAGAAATATCAATTAATGATGATGATGATGATGATGATGATGAT 840  
 QY 781 TAACTGGGCTTTTCAAGATGAGAAATATCAATTAATGATGATGATGATGATGATGATGATGAT 840  
 Db 781 TAACTGGGCTTTTCAAGATGAGAAATATCAATTAATGATGATGATGATGATGATGATGATGAT 840  
 QY 841 TCTTCCACAGCTCAAGATATCTACGAGAGATATCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
 Db 841 TCTTCCACAGCTCAAGATATCTACGAGAGATATCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
 QY 841 TCTTCCACAGCTCAAGATATCTACGAGAGATATCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
 Db 841 TCTTCCACAGCTCAAGATATCTACGAGAGATATCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
 QY 901 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 Db 901 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 QY 901 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 Db 901 TCTAAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 QY 961 CACATATCTGCTGAGGAGAACACACAGAGTATGCTGCTTAAACAGGAGCTCTGTA 1020  
 Db 961 CACATATCTGCTGAGGAGAACACACAGAGTATGCTGCTTAAACAGGAGCTCTGTA 1020  
 QY 961 CACATATCTGCTGAGGAGAACACACAGAGTATGCTGCTTAAACAGGAGCTCTGTA 1020  
 Db 961 CACATATCTGCTGAGGAGAACACACAGAGTATGCTGCTTAAACAGGAGCTCTGTA 1020  
 QY 1021 ATGGGCTGATGAGCAGTGTTCACAGACAGAGCTAATACCTAATGAGAGACATTAATA 1080  
 Db 1021 ATGGGCTGATGAGCAGTGTTCACAGACAGAGCTAATACCTAATGAGAGACATTAATA 1080  
 QY 1021 ATGGGCTGATGAGCAGTGTTCACAGACAGAGCTAATACCTAATGAGAGACATTAATA 1080  
 Db 1021 ATGGGCTGATGAGCAGTGTTCACAGACAGAGCTAATACCTAATGAGAGACATTAATA 1080  
 QY 1081 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Db 1081 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1081 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Db 1081 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1141 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGCTATTTGCTGTAATTTAA 1200  
 Db 1141 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGCTATTTGCTGTAATTTAA 1200  
 QY 1141 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGCTATTTGCTGTAATTTAA 1200  
 Db 1141 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGCTATTTGCTGTAATTTAA 1200  
 QY 1201 CACCTCTATACCTGAGATCCCT 1260  
 Db 1201 CACCTCTATACCTGAGATCCCT 1260  
 QY 1201 CACCTCTATACCTGAGATCCCT 1260  
 Db 1201 CACCTCTATACCTGAGATCCCT 1260  
 QY 1261 CAATATCAAGATTTATCTAACAACAATCTATTTGCTGGAACATGAAATTAACAGATT 1320  
 Db 1261 CAATATCAAGATTTATCTAACAACAATCTATTTGCTGGAACATGAAATTAACAGATT 1320  
 QY 1261 CAATATCAAGATTTATCTAACAACAATCTATTTGCTGGAACATGAAATTAACAGATT 1320  
 Db 1261 CAATATCAAGATTTATCTAACAACAATCTATTTGCTGGAACATGAAATTAACAGATT 1320  
 QY 1321 TGTGAAATCATTACACAGGCAATTTCTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 Db 1321 TGTGAAATCATTACACAGGCAATTTCTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 QY 1321 TGTGAAATCATTACACAGGCAATTTCTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 Db 1321 TGTGAAATCATTACACAGGCAATTTCTGAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 QY 1381 CCGAGTACGAAAGATATCAACAGGCTTCATTAACAAGACAGAGCAGATGAAATTAACAGATT 1440  
 Db 1381 CCGAGTACGAAAGATATCAACAGGCTTCATTAACAAGACAGAGCAGATGAAATTAACAGATT 1440  
 QY 1381 CCGAGTACGAAAGATATCAACAGGCTTCATTAACAAGACAGAGCAGATGAAATTAACAGATT 1440  
 Db 1381 CCGAGTACGAAAGATATCAACAGGCTTCATTAACAAGACAGAGCAGATGAAATTAACAGATT 1440  
 QY 1441 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 Db 1441 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 QY 1441 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 Db 1441 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 QY 1501 AGGAGAAAGAAATGCTGAGAGGTTGAGAGCCTATGAGAGCAGATGAAATTAACAGATT 1560  
 Db 1501 AGGAGAAAGAAATGCTGAGAGGTTGAGAGCCTATGAGAGCAGATGAAATTAACAGATT 1560  
 QY 1501 AGGAGAAAGAAATGCTGAGAGGTTGAGAGCCTATGAGAGCAGATGAAATTAACAGATT 1560  
 Db 1501 AGGAGAAAGAAATGCTGAGAGGTTGAGAGCCTATGAGAGCAGATGAAATTAACAGATT 1560  
 QY 1561 GCTGTATCT 1620  
 Db 1561 GCTGTATCT 1620  
 QY 1561 GCTGTATCT 1620  
 Db 1561 GCTGTATCT 1620  
 QY 1621 GGTAGAAGTTGAGACCAATCTCTCTTGAAGAGACTTAATGATGATGATGATGATGATGATGAT 1680  
 Db 1621 GGTAGAAGTTGAGACCAATCTCTCTTGAAGAGACTTAATGATGATGATGATGATGATGATGAT 1680  
 QY 1621 GGTAGAAGTTGAGACCAATCTCTCTTGAAGAGACTTAATGATGATGATGATGATGATGATGAT 1680  
 Db 1621 GGTAGAAGTTGAGACCAATCTCTCTTGAAGAGACTTAATGATGATGATGATGATGATGATGAT 1680  
 QY 1681 TGCCTACTGGAAGCAAGCACTTTTGTGAGAGAGGCTTTTCAATCAATCAACACTGC 1740  
 Db 1681 TGCCTACTGGAAGCAAGCACTTTTGTGAGAGAGGCTTTTCAATCAATCAACACTGC 1740  
 QY 1681 TGCCTACTGGAAGCAAGCACTTTTGTGAGAGAGGCTTTTCAATCAATCAACACTGC 1740  
 Db 1681 TGCCTACTGGAAGCAAGCACTTTTGTGAGAGAGGCTTTTCAATCAATCAACACTGC 1740  
 QY 1741 CTCAATTCATCTCTCATCTGCAATTAACGGAAGGCTGCTCTTACTTCACTTCACTGATGT 1800  
 Db 1741 CTCAATTCATCTCTCATCTGCAATTAACGGAAGGCTGCTCTTACTTCACTTCACTGATGT 1800



QY 1801 TCCAGATCCGAGCTCTATTAAACAGTCCACATCATGCAAGTTCTTCCGCTCCGAGCT 1860  
 DB 1801 TCCAGATCCGAGCTCTATTAAACAGTCCACATCATGCAAGTTCTTCCGCTCCGAGCT 1860  
 QY 1861 AGATGATCAATCCACAGTACTACTAAAGAAAGCGTGCATCGAACTGTAAGAGTCTAA 1920  
 DB 1861 AGATGATCAATCCACAGTACTACTAAAGAAAGCGTGCATCGAACTGTAAGAGTCTAA 1920  
 QY 1921 TGAATCATTTTATTTATTTATATGAACCATGCTATTAATTAATTAATTAATTAATTT 1980  
 DB 1921 TGAATCATTTTATTTATTTATATGAACCATGCTATTAATTAATTAATTAATTAATTT 1980  
 QY 1981 AATTTAACTCCTTATGTTACTTAACATCTTCTGTAACAGAAAGTCACTCCTGTTGGC 2040  
 DB 1981 AATTTAACTCCTTATGTTACTTAACATCTTCTGTAACAGAAAGTCACTCCTGTTGGC 2040  
 QY 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGTCATCTCTAAAGATTTTGTGTTGC 2100  
 DB 2041 GAGAAAGAGTCAATCTTGTGAAGACTTTTATGTCATCTCTAAAGATTTTGTGTTGC 2100  
 QY 2101 TGTTAAGTTTGGAAAAAGTTTATTTCTGTTTATTAACAGAGAGAAATGAGTTTGA 2160  
 DB 2101 TGTTAAGTTTGGAAAAAGTTTATTTCTGTTTATTAACAGAGAGAAATGAGTTTGA 2160  
 QY 2161 CGTCTTTTACTGTAATTTCAACTTATTAATTAAGAGAGAAAGTAAAGTGTGTAATAC 2220  
 DB 2161 CGTCTTTTACTGTAATTTCAACTTATTAATTAAGAGAGAAAGTAAAGTGTGTAATAC 2220  
 QY 2221 TTAACACTATCACAAGATGCCAAAAATGCTGAAAGTTTAAACAGTGCATGTTTCCAT 2280  
 DB 2221 TTAACACTATCACAAGATGCCAAAAATGCTGAAAGTTTAAACAGTGCATGTTTCCAT 2280  
 QY 2281 GCATCTTCATGATCATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 2340  
 DB 2281 GCATCTTCATGATCATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 2340  
 QY 2341 TTTTCTGTCATCAACAAACAAAGGATCATGTCATTTAATGAATTAATTAATTAAGTA 2400  
 DB 2341 TTTTCTGTCATCAACAAACAAAGGATCATGTCATTTAATGAATTAATTAATTAAGTA 2400  
 QY 2401 CATPACCAATGATTTTCAATGTCATCTTTTAAATGAGATGTAATTAATTAATTAATTA 2460  
 DB 2401 CATPACCAATGATTTTCAATGTCATCTTTTAAATGAGATGTAATTAATTAATTAATTA 2460  
 QY 2461 TCTAAATTCATAGGGTAGAATCACCTGTAAAGCTTGTGTTGATTTCTTAAAGTTATTA 2520  
 DB 2461 TCTAAATTCATAGGGTAGAATCACCTGTAAAGCTTGTGTTGATTTCTTAAAGTTATTA 2520  
 QY 2521 CTGTAACATATACCAAAAGAGAGCTGCTTGATTTAAATCTGTAAATTCAGATGAAAT 2580  
 DB 2521 CTGTAACATATACCAAAAGAGAGCTGCTTGATTTAAATCTGTAAATTCAGATGAAAT 2580  
 QY 2581 TTAACATGATGCTGTAAAAATTTTAAAGAGATGTCCTTTTCAACCAAGATTA 2640  
 DB 2581 TTAACATGATGCTGTAAAAATTTTAAAGAGATGTCCTTTTCAACCAAGATTA 2640  
 QY 2641 AACCTTTTAACTGTAAGTAAAGCTTCTTTTAAATCAAAATGSCAAATTTTATTAAG 2700  
 DB 2641 AACCTTTTAACTGTAAGTAAAGCTTCTTTTAAATCAAAATGSCAAATTTTATTAAG 2700  
 QY 2701 TGTGAGAGCCATGCAAGTGTATCTCAAAATTAAGATATCTGTTGAGATATCCAGAT 2760  
 DB 2701 TGTGAGAGCCATGCAAGTGTATCTCAAAATTAAGATATCTGTTGAGATATCCAGAT 2760  
 QY 2761 CTGTTTAAATGCTGTAAGTAAAGCTTCTTTTAAATCAAAATGSCAAATTTTATTAAG 2820  
 DB 2761 CTGTTTAAATGCTGTAAGTAAAGCTTCTTTTAAATCAAAATGSCAAATTTTATTAAG 2820  
 QY 2821 TTGAACATTAAGCAATTAACCAAAAGAGAGAAAGCCCAATTTTGTGTTCAAAATTTAGG 2880  
 DB 2821 TTGAACATTAAGCAATTAACCAAAAGAGAGAAAGCCCAATTTTGTGTTCAAAATTTAGG 2880

QY 2881 TTAACTTTTGAAGCAACTTTTATAGCCTTGAGCATGCGAGCCTGTAATCAGAT 2940  
 DB 2881 TTAACTTTTGAAGCAACTTTTATAGCCTTGAGCATGCGAGCCTGTAATCAGAT 2940  
 QY 2941 TTGCTATGAGGTTAATGAAGTACCAAGCTGCTGTAATTAAGATATGTTTCTCAGAT 3000  
 DB 2941 TTGCTATGAGGTTAATGAAGTACCAAGCTGCTGTAATTAAGATATGTTTCTCAGAT 3000  
 QY 3001 TTTCTGTTGACAGTTTATTTAGACATTCATATCAATTTGCAAAAGTACCAATGACCTC 3060  
 DB 3001 TTTCTGTTGACAGTTTATTTAGACATTCATATCAATTTGCAAAAGTACCAATGACCTC 3060  
 QY 3061 ATAAATACCTCTGCAAAATGCTTAAATTCATTTTCAATTTTATTTATCTGAGTCTG 3120  
 DB 3061 ATAAATACCTCTGCAAAATGCTTAAATTCATTTTCAATTTTATTTATCTGAGTCTG 3120  
 QY 3121 AAGCAATTCAGTAGGTCATTTGAATCAAGCTGCTGCTGATGCTGCTGCTGCTGCTG 3180  
 DB 3121 AAGCAATTCAGTAGGTCATTTGAATCAAGCTGCTGCTGATGCTGCTGCTGCTGCTG 3180  
 QY 3181 TTTCTCTTTTAGCCATTTTGTGTAAGACACAGATCTTCTGAAACATTTGTTCTGCTA 3240  
 DB 3181 TTTCTCTTTTAGCCATTTTGTGTAAGACACAGATCTTCTGAAACATTTGTTCTGCTA 3240  
 QY 3241 TTTGTTTATCAGTTTAAAGATCAGAGTTCATTTCTTGGACTGCTGCTATTTTCT 3300  
 DB 3241 TTTGTTTATCAGTTTAAAGATCAGAGTTCATTTCTTGGACTGCTGCTATTTTCT 3300  
 QY 3301 TACCTGAACCTTTTGCAGTTTCAAGTAAACCTCAGCTCAGGACTGCTATTTAGCTCTC 3360  
 DB 3301 TACCTGAACCTTTTGCAGTTTCAAGTAAACCTCAGCTCAGGACTGCTATTTAGCTCTC 3360  
 QY 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387  
 DB 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387

RESULT 5  
 ABA94344  
 ID ABA94344 standard; DNA, 3387 BP.  
 XX ABA94344;  
 AC 26-MAR-2002 (first entry)  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human cyclooxygenase-2 (COX-2) protein encoding DNA.  
 XX  
 KW Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;  
 XX inflammation; central nervous system; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 98..1912  
 FT /\*tag= a  
 FT /transl\_except= (pos: 589..591, aa: Glu)  
 FT /product= "COX-1"  
 FT  
 EN W0200111026-A1.  
 XX  
 PD 15-FEB-2001.  
 XX  
 PF 04-AUG-2000; 2000WO-US019565.  
 XX  
 PR 06-AUG-1999; 99US-0147601P.  
 XX  
 PA (SEAR) SEARLE & CO G D.  
 XX  
 PI Gliese JK;  
 XX  
 DR WPI, 2002-113777/15.  
 DR P-PSDB; ABB07244.  
 XX

Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful for identifying drugs that can reduce inflammation in dogs, and screening selective inhibitors of cyclooxygenase-2 protein.

Disclosure; Page 94-97; 122pp; English.

The invention relates to genes that encode canine cyclooxygenase (COX)-1 or COX-2 proteins. The COX proteins, especially COX-2 is useful for diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its fragment is useful for identifying a test material which has the ability to inhibit, suppress, modulate, or maintain canine COX-2 activity. The COX-1 and COX-2 polynucleotides are useful for determining an association between a polymorphism and a trait. COX-2 cDNA molecules and methods provided are also useful for diagnosing or prognosing COX-2 related condition such as arthritis, cancer, neoplasia, inflammation or central nervous system disorder in a dog. The present sequence represents a human COX-2 protein encoding DNA

Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 6; Length 3387;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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1 GTCCAGGAACCTCCTCAGCAGCGCTCTCTCAGCTCCACAGCCAGAGCCCTCAGACAGCA 60
1 GTCCAGGAACCTCCTCAGCAGCGCTCTCTCAGCTCCACAGCCAGAGCCCTCAGACAGCA 60
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121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
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181 CGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
241 ATTCTATGAGAAAGTCTGCTCAACACCGGAATTTTGAACAAGATTAATTTTCTGAA 300
241 ATTCTATGAGAAAGTCTGCTCAACACCGGAATTTTGAACAAGATTAATTTTCTGAA 300
301 ACCCATCTCCAAACAGTGCATACATCTTACCCCTTCAAGGATTTTGAAGCTTGT 360
301 ACCCATCTCCAAACAGTGCATACATCTTACCCCTTCAAGGATTTTGAAGCTTGT 360
361 GAATACATTCCTCTCTCTGAAATGCAATTAATGATGATGATGATGATGATGATGATGAT 420
361 GAATACATTCCTCTCTCTGAAATGCAATTAATGATGATGATGATGATGATGATGATGAT 420
421 TTGATTTGACAGTCCACCACTTACATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 480
421 TTGATTTGACAGTCCACCACTTACATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 480
481 CTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
481 CTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
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541 CTTGAGTGTCAAGTGTAAAGAGAGCTTCTCTGATTCATTAATGAGATTTGGAAAAATTTGCT 600
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601 TCTAAGAGAAAGTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
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661 CGAGCACTTACGACAGAGTTTTCAGAGAGATCATTAAGAGAGAGAGAGAGAGAGAGAG 720
721 CGAGGCTGGGCGATGAGGAGGAGCTTAATCATATTATTAAGAGAGAGAGAGAGAGAG 780
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781 TAAATGCGCTTTTCAAGAGATGAGAAAGTAAATATCATGATTAATGATGAGAGATGTA 840
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1621 GGTAGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
1681 TGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
1681 TGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
1741 CTAATTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
1741 CTAATTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
1801 TCCAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
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PS Disclosure; SEQ ID NO 12051; 872bp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end and genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cyostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;

Query Match 99.8%; Score 3379; DB 7; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 5; Indels 0; Gaps 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCAGAACTCTCTGAGACGCGCTCTCAGCTCCACAGCAGCGCCTTACAGACGA 60  
 DB 1 GTCCAGAACTCTCTGAGACGCGCTCTCAGCTCCACAGCAGCGCCTTACAGACGA 60  
 QY 61 AAGCCTACCCCG 120  
 DB 61 AAGCCTACCCCG 120  
 QY 121 GTCCGCGGTCCTGGCGCTCAGCATACAGCAAACTCTGCTGTCCACCGCAATGCAAA 180  
 DB 121 GTCCGCGGTCCTGGCGCTCAGCATACAGCAAACTCTGCTGTCCACCGCAATGCAAA 180  
 QY 121 GTCCGCGGTCCTGGCGCTCAGCATACAGCAAACTCTGCTGTCCACCGCAATGCAAA 180  
 DB 121 GTCCGCGGTCCTGGCGCTCAGCATACAGCAAACTCTGCTGTCCACCGCAATGCAAA 180  
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 DB 181 CCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
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 DB 181 CCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
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 DB 241 ATTCTATGAGAAATGCTGCTCAACCGGAAATTTTGAACAAGATTAATTTCTGAA 300  
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 QY 301 ACCCACTCCAAACAGAGTGACATACATCTTACCACTTCAAGGAAATTTGGAAGCTGT 360  
 DB 301 ACCCACTCCAAACAGAGTGACATACATCTTACCACTTCAAGGAAATTTGGAAGCTGT 360  
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 DB 361 GATAAATATTCCTCTCTGAAATGAAATTAAGATTAAGTGTGATGATGATGATGATGAT 420  
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 DB 421 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
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 DB 601 TCTTAAGAGAAAGTCAATCCCTGATCCCAAGGAGCTCAAAATGATGATGATGATGATGAT 660

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 DB 901 TCTACGTTTGT 960  
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 DB 961 CACCAATCTGGCTGGGGAACCAACAGAGATGATGATGATGATGATGATGATGATGATGAT 1020  
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 DB 1021 ATGGGATGATGAGCAGTGTGTCAGACAGAGCTAATTAATGATGATGATGATGATGAT 1080  
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 DB 1081 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1081 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
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 DB 1561 GCTGTATCTGCTTCTGCTGATGAAAGAGCTGCGGAGATGATGATGATGATGATGAT 1620  
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 DB 1741 CTCATTCAGTCTCTCATCTGCAATTAACGTGAAGGAGCTGCTCTTCACTTCAGTGT 1800

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Db      1801 TCCAGATCCAGAGCTATTAATAACAGTACCATCAATGCAAGTCTTCCCGCTCCGAGCT 1860
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Db      1861 AGATGATCAATCCCAAGCTACTACTTAAGAAAGCGTGCATGAACTGTAGAAGTCTAA 1920
Qy      1921 TGAATCAATTTATTTATTAATGAAACAGTCTATTAATTAATTAATTAATTAATTAAT 1980
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Qy      1981 AATTAACCTCTTAATGTTACTTAACATCTTCTGTAACAGAAAGTCACTCCGTGTGGG 2040
Db      1981 AATTAACCTCTTAATGTTACTTAACATCTTCTGTAACAGAAAGTCACTCCGTGTGGG 2040
Qy      2041 GGAAGAAGGCTACTTCTGTGAAGACTTTTATGTCTACTCTTAAGATTTTGTGTGCTC 2100
Db      2041 GGAAGAAGGCTACTTCTGTGAAGACTTTTATGTCTACTCTTAAGATTTTGTGTGCTC 2100
Qy      2101 TGTAAAGTTTGGAAAAAGTTTATCTGTGTTTAAACGAGAGAAATAGATTGTA 2160
Db      2101 TGTAAAGTTTGGAAAAAGTTTATCTGTGTTTAAACGAGAGAAATAGATTGTA 2160
Qy      2161 CGTCTTTTACTGTAATTTCACTTAATTAATGAGAGCAAGTAAGATGTTTGAATC 2220
Db      2161 CGTCTTTTACTGTAATTTCACTTAATTAATGAGAGCAAGTAAGATGTTTGAATC 2220
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Db      2281 GCATCTTCCATGATGATAGAGTAAGTAACTGTTGAAATTTTAAAGTCTTTGGGTA 2340
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Qy      2521 CTTTGATACATACCAAAAAAGAGCTGTCTGATTTAAATCTGTAATCAGATGAAT 2580
Db      2521 CTTTGATACATACCAAAAAAGAGCTGTCTGATTTAAATCTGTAATCAGATGAAT 2580
Qy      2581 TTACTACAAATGCTGTTTAAATATTTTAAAGTGAATGCTGTTTCAACCAAGATTA 2640
Db      2581 TTACTACAAATGCTGTTTAAATATTTTAAAGTGAATGCTGTTTCAACCAAGATTA 2640
Qy      2641 AACCTTTTAGTGATGCTTAAACCTCTTTAAATCAAAATGCCAAATTTATTAAG 2700
Db      2641 AACCTTTTAGTGATGCTTAAACCTCTTTAAATCAAAATGCCAAATTTATTAAG 2700
Qy      2701 TGGTGAGCCACTGCAAGTATATCTCAAAATAGAAATTCGTTGAGATATTCAGAT 2760
Db      2701 TGGTGAGCCACTGCAAGTATATCTCAAAATAGAAATTCGTTGAGATATTCAGAT 2760
Qy      2761 CTGTTTATATGCTGTGTAACTGTAAACCCCATACCCGCCCAAAAGGGGTCTTACC 2820
Db      2761 CTGTTTATATGCTGTGTAACTGTAAACCCCATACCCGCCCAAAAGGGGTCTTACC 2820
Qy      2821 TTGAACATTAAGCATATACCAAGAGAAAGCCCAATTTATGTTTCCAAATTTAGGT 2880

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Db      2821 TTGAACATTAAGCATATACCAAGAGAAAGCCCAATTTATGTTTCCAAATTTAGGT 2880
Qy      2881 TTAACTTTTGAAGCAAACTTTTATGACCTGTGCACTGAGACCTGTCTAGAT 2940
Db      2881 TTAACTTTTGAAGCAAACTTTTATGACCTGTGCACTGAGACCTGTCTAGAT 2940
Qy      2941 TTTGCTAGAGGTTAATGAAAGTACCAAGCTGTCTGTAATTAAGATGTTTCTAGAT 3000
Db      2941 TTTGCTAGAGGTTAATGAAAGTACCAAGCTGTCTGTAATTAAGATGTTTCTAGAT 3000
Qy      3001 TTTTCTGTACAGTTTAAATTTAGCAGTCAATTCACATTTGCAAAAGTAGCAATGAC 3060
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Db      3061 ATAAATACCTCTTCAAAATGCTTAATTCATTTCAATTTCAATTTATTTATCTGACT 3120
Qy      3121 AAGCCAAATTCAGTAGGTCATGGAATCAAGCTGCTGCTGATGCTGCTCTTCT 3180
Db      3121 AAGCCAAATTCAGTAGGTCATGGAATCAAGCTGCTGCTGATGCTGCTCTTCT 3180
Qy      3181 TTTCTCTTTTTCAGCAATTTTCTGTAAGACACAGTCTTCTCAAACTTGTCTCTTA 3240
Db      3181 TTTCTCTTTTTCAGCAATTTTCTGTAAGACACAGTCTTCTCAAACTTGTCTCTTA 3240
Qy      3241 TTTTGTCTTACTAGTTTAAATGATCAGAGTTCATTTCTTTGACCTGCTATTTTCT 3300
Db      3241 TTTTGTCTTACTAGTTTAAATGATCAGAGTTCATTTCTTTGACCTGCTATTTTCT 3300
Qy      3301 TACCTGAACCTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGGACTGTATTAAGCTCC 3360
Db      3301 TACCTGAACCTTTTGCAGTTTTCAGGTAAACCTCAGCTCAGGACTGTATTAAGCTCC 3360
Qy      3361 TTAAAGAGTTTAAAAAAG 3387
Db      3361 TTAAAGAGTTTAAAAAAG 3387

RESULT 7
ACF63365
ID ACF63365 standard; DNA; 3387 BP.
XX
AC ACF63365;
XX
DT 09-OCT-2003 (first entry)
XX
DE Human cyclooxygenase 2 gene SEQ ID NO:87.
XX
KW Human; pharmacological; hypotensive; antihypertensive; vasodilator; laxative;
KW dermatological; antidepressant; tranquilizer; antiinflammatory; eczema;
KW antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;
KW gynaecological; virucide; vulnery; antidiabetic; antiparasitic; cold;
KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
KW constipation; headache; seizure; multiple sclerosis; polymyositis;
KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatic;
KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
KW skin disorder; gene; ds.
XX
OS Homo sapiens.
XX
WO2003006478-A1.
XX
PD 23-JAN-2003.
XX
PE 10-JUL-2002; 2002MO-US021664.
XX
PR 10-JUL-2001; 2001US-0303820P.

```

XX (OLIG-) OLIGOS ETC INC.  
 PA Dale RMK, Arrow A, Thompson T;  
 XX WPI: 2003-221709/21.  
 XX  
 PT Composition with a modified oligonucleotide useful for treating a patient  
 PT with a pathological disorder such as abnormal appetite, hypertension,  
 PT eczema, anxiety, stress, and cancer.  
 XX  
 PS Claim 6: Page 83-85; 173pp; English.  
 CC  
 CC The present invention describes a composition (I) suitable for  
 CC administration in a mammal, which comprises a modified oligonucleotide  
 CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups  
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the  
 CC modified oligonucleotide is complementary to a region of a gene  
 CC associated with a pathological disorder. Also described: (1) a  
 CC nutritional supplement comprising (II); and (2) a cosmetic composition  
 CC comprising (II), where the modified oligonucleotide is complementary to a  
 CC region of a gene associated with a skin disorder. (I) and (II) can have  
 CC hypotensive, antihypertensive, vasodilatory, dermatological, antidiabetic,  
 CC tranquilizer, antiinflammatory, antitumor, laxative, antimigraine,  
 CC neuroprotective, antiparkinsonian, analgesic, gynecological, vituocide,  
 CC vulnerary, antiarthritic, antipruritic, antimicrobial, cyrostatic and  
 CC litholytic activities. (1) can be used for treating a patient with a  
 CC pathological disorder selected from abnormal appetite, hypertension,  
 CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,  
 CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative  
 CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,  
 CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,  
 CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),  
 CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,  
 CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatics,  
 CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant  
 CC melanoma, and malignant nasal polyps. The nutritional supplement is  
 CC useful for supplementing the diet of an individual, and the cosmetic  
 CC composition is useful for improving the appearance of the skin in an  
 CC individual with a skin disorder. ACF63279 to ACF63410 represent  
 CC nucleotide sequence given in the exemplification of the present invention  
 XX  
 SQ Sequence 3387 BP; 1010 A; 712 C; 633 G; 1032 T; 0 U; 0 Other;  
 Query Match 99.8%; Score 3379; DB 7; Length 3387;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3382; Conservativity 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GTCCAGGAACTCCTCGACGCGGCTCTGAGCTCCACAGCGAGCGCTCGACAGCA 60  
 DB 1 GTCCAGGAACTCCTCGACGCGGCTCTGAGCTCCACAGCGAGCGCTCGACAGCA 60  
 QY 61 AAGCTTACCCCGCGCGCGGCTCTGAGCTCCACAGCGAGCGCTCGACAGCA 120  
 DB 61 AAGCTTACCCCGCGCGCGGCTCTGAGCTCCACAGCGAGCGCTCGACAGCA 120  
 QY 121 GTGCGGCGTCTGCGCGCTGACGCAATGCGGATGCTGCTGCTGCTGCTGCTGCT 180  
 DB 121 GTGCGGCGTCTGCGCGCTGACGCAATGCGGATGCTGCTGCTGCTGCTGCTGCT 180  
 QY 121 GTGCGGCGTCTGCGCGCTGACGCAATGCGGATGCTGCTGCTGCTGCTGCTGCT 180  
 DB 121 GTGCGGCGTCTGCGCGCTGACGCAATGCGGATGCTGCTGCTGCTGCTGCTGCT 180  
 QY 181 CGAGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 DB 181 CGAGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 QY 181 CGAGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 DB 181 CGAGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 QY 241 ATTCTATGAGAGAAATGCTCAACACCGAATTTTTCAGCAAGATTAATTTTTCGAA 300  
 DB 241 ATTCTATGAGAGAAATGCTCAACACCGAATTTTTCAGCAAGATTAATTTTTCGAA 300  
 QY 301 ACCCACTCCAAACAGTGCATACATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
 DB 301 ACCCACTCCAAACAGTGCATACATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
 QY 361 GAATTAATTCCTCTCTGGAATGCAATTATGATGATGATGATGATGATGATGATGAT 420

DB 361 GAATTAATTCCTCTCTGGAATGCAATTATGATGATGATGATGATGATGATGATGAT 420  
 QY 421 TTTGATTAAGAGTCCACCAACTTACATGCTGATGCTGATGCTGATGCTGATGCTGAT 480  
 DB 421 TTTGATTAAGAGTCCACCAACTTACATGCTGATGCTGATGCTGATGCTGATGCTGAT 480  
 QY 481 CTCTAACCT 540  
 DB 481 CTCTAACCT 540  
 QY 541 CTCTAACCT 600  
 DB 541 CTCTAACCT 600  
 QY 601 TCTTAAGAGAGAGTTCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 660  
 DB 601 TCTTAAGAGAGAGTTCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 660  
 QY 661 CCAGGAGTTCAGGAGGAGTTCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 720  
 DB 661 CCAGGAGTTCAGGAGGAGTTCATCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 720  
 QY 721 CGGCGTGGGCGATGCGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 780  
 DB 721 CGGCGTGGGCGATGCGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 780  
 QY 781 TAAATCGCGCTTTTCAAG 840  
 DB 781 TAAATCGCGCTTTTCAAG 840  
 QY 841 TCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 900  
 DB 841 TCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 900  
 QY 901 TCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 960  
 DB 901 TCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 960  
 QY 961 CACATTCGCTGAG 1020  
 DB 961 CACATTCGCTGAG 1020  
 QY 1021 AAGGAGTGAATGAG 1080  
 DB 1021 AAGGAGTGAATGAG 1080  
 QY 1081 GATTTGATTAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 DB 1081 GATTTGATTAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1141 CCAG 1200  
 DB 1141 CCAG 1200  
 QY 1201 CACCTCTATCACTGAG 1260  
 DB 1201 CACCTCTATCACTGAG 1260  
 QY 1261 CAATATCAAG 1320  
 DB 1261 CAATATCAAG 1320  
 QY 1321 TGTGATATCAATCAAG 1380  
 DB 1321 TGTGATATCAATCAAG 1380  
 QY 1381 CGAGTACAG 1440  
 DB 1381 CGAGTACAG 1440  
 QY 1441 TTTTAAATGAGTACCGGAG 1500

Db 1441 TTTAATGAGTACCGGAAAGCTTTATGCTGAAGCCCTATGAATCATTTGGAACCTTAC 1500  
 QY 1501 AGAGAGAAAAGAAATGTCTGAGAGAGTTGGAAGCACTCTATGTGACATGAGTGTGGA 1560  
 Db 1501 AGAGAGAAAAGAAATGTCTGAGAGAGTTGGAAGCACTCTATGTGACATGAGTGTGGA 1560  
 QY 1561 GCGTATCCGCGCTCTGTGTGAGAAAAGCTGGGCGAGATGCCATCTTTGGTGAACCAT 1620  
 Db 1561 GCGTATCCGCGCTCTGTGTGAGAAAAGCTGGGCGAGATGCCATCTTTGGTGAACCAT 1620  
 QY 1621 GGTAGAGTTGGAGACCACTTCTCCTTGAAGAGCTTATGGGTAATGTATATGTTCTCC 1680  
 Db 1621 GGTAGAGTTGGAGACCACTTCTCCTTGAAGAGCTTATGGGTAATGTATATGTTCTCC 1680  
 QY 1681 TGCCTATCTGGAAAGCAAGCACTTTGGTGAAGAGTGGGTTTCAAAATCATCAACATGC 1740  
 Db 1681 TGCCTATCTGGAAAGCAAGCACTTTGGTGAAGAGTGGGTTTCAAAATCATCAACATGC 1740  
 QY 1741 CTCAATTCAGTCTCATCTGCAATTAAGTGAAGGGCTGTCCCTTACTCTTCATTCAGTGT 1800  
 Db 1741 CTCAATTCAGTCTCATCTGCAATTAAGTGAAGGGCTGTCCCTTACTCTTCATTCAGTGT 1800  
 QY 1801 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTGTCTCCCGCTCCGACAT 1860  
 Db 1801 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTGTCTCCCGCTCCGACAT 1860  
 QY 1861 AGATGATATCAATCCCAAGTACTCTAAAGAGAGTTCGAGTGAAGTGAAGTCTTAA 1920  
 Db 1861 AGATGATATCAATCCCAAGTACTCTAAAGAGAGTTCGAGTGAAGTGAAGTCTTAA 1920  
 QY 1921 TGATCATTTATTTATTTATTAATGAACAGATGCTTATTAATTTATTAATAATATTT 1980  
 Db 1921 TGATCATTTATTTATTTATTAATGAACAGATGCTTATTAATTTATTAATAATATTT 1980  
 QY 1981 ATATTTAACTCCTTATGTTACTTAAACATCTCTGTGAAGAGAGTCAAGTCTGTCGG 2040  
 Db 1981 ATATTTAACTCCTTATGTTACTTAAACATCTCTGTGAAGAGAGTCAAGTCTGTCGG 2040  
 QY 2041 GAGAAAGAGTCAATCTGTGAAGAGCTTTATGTCACACTCTAAAGATTTTGGCTGTGC 2100  
 Db 2041 GAGAAAGAGTCAATCTGTGAAGAGCTTTATGTCACACTCTAAAGATTTTGGCTGTGC 2100  
 QY 2101 TGTAAAGTTGGAGAAACAGTTTATCTGTATTATTAACAGAGAGAAATGAGTTTGA 2160  
 Db 2101 TGTAAAGTTGGAGAAACAGTTTATCTGTATTATTAACAGAGAGAAATGAGTTTGA 2160  
 QY 2161 CGTCTTTTACTGTAATTTCACTTATATTAATTAAGAGAGAAAGTGTTCGAT 2220  
 Db 2161 CGTCTTTTACTGTAATTTCACTTATATTAATTAAGAGAGAAAGTGTTCGAT 2220  
 QY 2221 TTTAAACATTCACAGAGTGGCAAAATGTGAAAGTTTTACACTGTGCAATGTTCCAT 2280  
 Db 2221 TTTAAACATTCACAGAGTGGCAAAATGTGAAAGTTTTACACTGTGCAATGTTCCAT 2280  
 QY 2281 GCATCTTCCATGATGCAATTAAGAGTAACTGAATGTTGAATTTTAAAGTCTTTGGGTA 2340  
 Db 2281 GCATCTTCCATGATGCAATTAAGAGTAACTGAATGTTGAATTTTAAAGTCTTTGGGTA 2340  
 QY 2341 TTTTCTGTGATCAACCAAAACAGTATCAGTGCATTAATTAATGAATTTTAAATTAAGA 2400  
 Db 2341 TTTTCTGTGATCAACCAAAACAGTATCAGTGCATTAATTAATGAATTTTAAATTAAGA 2400  
 QY 2401 CATTTACAGTAATTTTCAATGTTCTAATTTTAAATCAGCAATGAACAAATATTTGAAT 2460  
 Db 2401 CATTTACAGTAATTTTCAATGTTCTAATTTTAAATCAGCAATGAACAAATATTTGAAT 2460  
 QY 2461 TCTAAATTCATAGGTAATCACTGTAATTAAGTGAATGTTGATTTCTTAAAGTTTAA 2520  
 Db 2461 TCTAAATTCATAGGTAATCACTGTAATTAAGTGAATGTTGATTTCTTAAAGTTTAA 2520  
 QY 2521 CTGTGATATATACCAAAAGAGAGTCTGTGATTTAAATCTGTAAATCATGATGAAT 2580  
 Db 2521 CTGTGATATATACCAAAAGAGAGTCTGTGATTTAAATCTGTAAATCATGATGAAT 2580

QY 2581 TTACTAGAAATGCTGTTTAAATATTTTATTAAGTATGTTCTTTTACCAAGAGTATA 2640  
 Db 2581 TTACTAGAAATGCTGTTTAAATATTTTATTAAGTATGTTCTTTTACCAAGAGTATA 2640  
 QY 2641 AACCTTTTATGAGTACGTTTAAACCTTCCTTTTAAATCAAAATGCAAAATTTATTAAG 2700  
 Db 2641 AACCTTTTATGAGTACGTTTAAACCTTCCTTTTAAATCAAAATGCAAAATTTATTAAG 2700  
 QY 2701 TGTGAGAGCACTGAGTGTATCTCAAAATTAAGAAATCTGTGAGATATTCAGAAAT 2760  
 Db 2701 TGTGAGAGCACTGAGTGTATCTCAAAATTAAGAAATCTGTGAGATATTCAGAAAT 2760  
 QY 2761 CTGTTTATATGCTGTGTAACTGTAAAAACCCCATTAACCCCGCAAAAGGGTCTACCC 2820  
 Db 2761 CTGTTTATATGCTGTGTAACTGTAAAAACCCCATTAACCCCGCAAAAGGGTCTACCC 2820  
 QY 2821 TTGAACATTAAGCAATTAACCAAGAGAGAAAGCCCAATTTATGTTTCCAAATTTAGGCT 2880  
 Db 2821 TTGAACATTAAGCAATTAACCAAGAGAGAAAGCCCAATTTATGTTTCCAAATTTAGGCT 2880  
 QY 2881 TTAAACCTTTTGAAGCAAACTTTTATAGCCTGTGTGACAGTCAAGCTGTGACTCAGAT 2940  
 Db 2881 TTAAACCTTTTGAAGCAAACTTTTATAGCCTGTGTGACAGTCAAGCTGTGACTCAGAT 2940  
 QY 2941 TTTGCTATGAGTAAATGAATTAACCAAGCTGTGTGAAATACGATATGTTTCTCAGAT 3000  
 Db 2941 TTTGCTATGAGTAAATGAATTAACCAAGCTGTGTGAAATACGATATGTTTCTCAGAT 3000  
 QY 3001 TTTCTGTGTATCAGTTTAAATTTAGCAGTCCATATCAATTCGAAAGTAGAATGACCTC 3060  
 Db 3001 TTTCTGTGTATCAGTTTAAATTTAGCAGTCCATATCAATTCGAAAGTAGAATGACCTC 3060  
 QY 3061 ATTAATAATCTCTTCAAAATGCTTAAATTCATTTACACATTAATTTTATCTCAGTCTG 3120  
 Db 3061 ATTAATAATCTCTTCAAAATGCTTAAATTCATTTACACATTAATTTTATCTCAGTCTG 3120  
 QY 3121 AAGCCATTCAGTATGAGTGAATTCGAATCAAGCTGTGCTGATGCTGTCTTCT 3180  
 Db 3121 AAGCCATTCAGTATGAGTGAATTCGAATCAAGCTGTGCTGATGCTGTCTTCT 3180  
 QY 3181 TTTCTTCTTTTAGCATTGTTGCTAAGAGACAGTCTTCTCAACACTGCTTCTCTCTA 3240  
 Db 3181 TTTCTTCTTTTAGCATTGTTGCTAAGAGACAGTCTTCTCAACACTGCTTCTCTCTA 3240  
 QY 3241 TTTTGTATTATCAGTTTAAAGTCAAGTTCATTTCTTTGAGTCTGCTCATATTTTCT 3300  
 Db 3241 TTTTGTATTATCAGTTTAAAGTCAAGTTCATTTCTTTGAGTCTGCTCATATTTTCT 3300  
 QY 3301 TACCTGAACCTTTTGCAAGTTTTCAGGTAACCTTCAGTCAAGACTGCTATTTAGCTCTC 3360  
 Db 3301 TACCTGAACCTTTTGCAAGTTTTCAGGTAACCTTCAGTCAAGACTGCTATTTAGCTCTC 3360  
 QY 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387  
 Db 3361 TTAAGAGATTAATAAAAAAAAAAAG 3387

RESULT 8  
 AAA34995  
 ID AAA34995 standard; DNA; 15240 BP.  
 XX  
 AC AAA34995;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2684.  
 XX  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;







```
QY 1321 TGTGATCATTCACGAGCAAAATGCTG3CAGGGTGTGCTGTAGGATGTTCCACC 1380
DB |||||
QY 3721 TGTGATCATTCACGAGCAAAATGCTG3CAGGGTGTGCTGTAGGATGTTCCACC 3780
DB |||||
QY 1381 CGCAGTACGAAAGATATCAGAGCTTCCATTGACCGAGCAGGACATGAAATACCAGTC 1440
DB |||||
QY 3781 CGCAGTACGAAAGATATCAGAGCTTCCATTGACCGAGCAGGACATGAAATACCAGTC 3840
DB |||||
QY 1441 TTTTATGAGTACCGCAAAACGCTTATGCTGAAGCCCTATGAATCATTTGAAGACTTAC 1500
DB |||||
QY 3841 TTTTATGAGTACCGCAAAACGCTTATGCTGAAGCCCTATGAATCATTTGAAGACTTAC 3900
DB |||||
QY 1501 AGGAGAAAAGAAATGTCTGACAGTGGAGCACTCTATGCTGACATGATGCTGTGA 1560
DB |||||
QY 3901 AGGAGAAAAGAAATGTCTGACAGTGGAGCACTCTATGCTGACATGATGCTGTGA 3960
DB |||||
QY 1561 GCTGATCCTGCTCTGCTGTAGAAAAGCTGCGGCAATGCTGCTTGTGTAACCAT 1620
DB |||||
QY 3961 GCTGATCCTGCTCTGCTGTAGAAAAGCTGCGGCAATGCTGCTTGTGTAACCAT 4020
DB |||||
QY 1621 GGTAGAGTGGAGCACCATTCTCTTGAAGAAGACTTATGAGTAAATGTTATGTTCTCC 1680
DB |||||
QY 4021 GGTAGAGTGGAGCACCATTCTCTTGAAGAAGACTTATGAGTAAATGTTATGTTCTCC 4080
DB |||||
QY 1681 TGCCTACTGGAAGCCCAAGACTTTTGTGAGAAAGTGG3TTCATAATCATCAACACTGC 1740
DB |||||
QY 4081 TGCCTACTGGAAGCCCAAGACTTTTGTGAGAAAGTGG3TTCATAATCATCAACACTGC 4140
DB |||||
QY 1741 CTCAATTCAGTCTCTCATCTGCAATAGTGAAGGGCTGCTCCCTTACTTCAATTCAGTGT 1800
DB |||||
QY 4141 CTCAATTCAGTCTCTCATCTGCAATAGTGAAGGGCTGCTCCCTTACTTCAATTCAGTGT 4200
DB |||||
QY 1801 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTTCTCCGCTCCGAGCT 1860
DB |||||
QY 4201 TCCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTTCTCCGCTCCGAGCT 4260
DB |||||
QY 1861 AGATGATATCAATCCCAAGTACTATCTAAAGAAAGGCTGCACTGAATCTGAAAGTCTAA 1920
DB |||||
QY 4261 AGATGATATCAATCCCAAGTACTATCTAAAGAAAGGCTGCACTGAATCTGAAAGTCTAA 4320
DB |||||
QY 1921 TGATCATTTTATTTATTTATTTATGAAACGATGCTTATTTATTTATTTATTTATTTATTT 1980
DB |||||
QY 4321 TGATCATTTTATTTATTTATTTATGAAACGATGCTTATTTATTTATTTATTTATTTATTT 4380
DB |||||
QY 1981 ATATTTAACTCCTTATGTTACTTAAACATCTTCTGTAACAGAAAGTCAAGTCTGTTGCG 2040
DB |||||
QY 4381 ATATTTAACTCCTTATGTTACTTAAACATCTTCTGTAACAGAAAGTCAAGTCTGTTGCG 4440
DB |||||
QY 2041 GAGAAAGAGTCAATCTTGTGAAGAATTTATGTCATCACTCTAAAGATTTTGTGTTGC 2100
DB |||||
QY 4441 GAGAAAGAGTCAATCTTGTGAAGAATTTATGTCATCACTCTAAAGATTTTGTGTTGC 4500
DB |||||
QY 2101 TGTAAAGTTTGGAAAAAGTTTTTATCTGTTTATTTAAACAGAGAAATGAGTTTGA 2160
DB |||||
QY 4501 TGTAAAGTTTGGAAAAAGTTTTTATCTGTTTATTTAAACAGAGAAATGAGTTTGA 4560
DB |||||
QY 2161 CGTCTTTTAACTTGAATTTCACTTATTTAAGACGAAAGTAAAGATTTTGAATAC 2220
DB |||||
QY 4561 CGTCTTTTAACTTGAATTTCACTTATTTAAGACGAAAGTAAAGATTTTGAATAC 4620
DB |||||
QY 2221 TTTAAACCTATCACAAGATGCAAAATGCTGAAAGTTTTTACATGTCGATGTTTCAAT 2280
DB |||||
QY 4621 TTTAAACCTATCACAAGATGCAAAATGCTGAAAGTTTTTACATGTCGATGTTTCAAT 4680
DB |||||
QY 2281 GCATCTTCCATGATGCAATGAGTAACTATGTTTGAATTTTAAAGTACTTTGGGTA 2340
DB |||||
QY 4681 GCATCTTCCATGATGCAATGAGTAACTATGTTTGAATTTTAAAGTACTTTGGGTA 4740
DB |||||
QY 2341 TTTTCTGTCATCAACAAACAGGTATCAGTCAATTAATAATGATTAATTTAAATTGA 2400
DB |||||
QY 4741 TTTTCTGTCATCAACAAACAGGTATCAGTCAATTAATAATGATTAATTTAAATTGA 4800
DB |||||

QY 2401 CATPACAGTAAATTCATGCTACTTTTAAATGACGATGAAACAAATTAATTTGAATT 2460
DB |||||
QY 4801 CATPACAGTAAATTCATGCTACTTTTAAATGACGATGAAACAAATTAATTTGAATT 4860
DB |||||
QY 2461 TCTAAATTCATAGGGTAGAATCACCTGTAAAGCTTGTGTTATTTCTTAAAGTTATTA 2520
DB |||||
QY 4861 TCTAAATTCATAGGGTAGAATCACCTGTAAAGCTTGTGTTATTTCTTAAAGTTATTA 4920
DB |||||
QY 2521 CTTGTACATATPACAAAAAGAAAGCTGTCTGTGATTTAAATCTGTAAATCAGATGAAT 2580
DB |||||
QY 4921 CTTGTACATATPACAAAAAGAAAGCTGTCTGTGATTTAAATCTGTAAATCAGATGAAT 4980
DB |||||
QY 2581 TTACTACAAATGCTGTTTAAATATTTATTAAGATGCTTCTTTTACCCAAAGTATA 2640
DB |||||
QY 4981 TTACTACAAATGCTGTTTAAATATTTATTAAGATGCTTCTTTTACCCAAAGTATA 5040
DB |||||
QY 2641 AACCTTTTATGATGCTGTAAACCTTCTTTTAAATCAAAATGCCAAATTTATTAAG 2700
DB |||||
QY 5041 AACCTTTTATGATGCTGTAAACCTTCTTTTAAATCAAAATGCCAAATTTATTAAG 5100
DB |||||
QY 2701 TGTGAGACCACTGACAGTGTATCTCAAAATPAGAAATCCTGTTGAATATTCAGAT 2760
DB |||||
QY 5101 TGTGAGACCACTGACAGTGTATCTCAAAATPAGAAATCCTGTTGAATATTCAGAT 5160
DB |||||
QY 2761 CTGTTTATATGCTGTGTAACATGTAATAAACCCATPACCCGCAAAAGGGTCTTACC 2820
DB |||||
QY 5161 CTGTTTATATGCTGTGTAACATGTAATAAACCCATPACCCGCAAAAGGGTCTTACC 5220
DB |||||
QY 2821 TTGAACATTAAGCAATTAACAAAGAGAAAGCCCAATTTATGTTTCAAAATTTAGGGT 2880
DB |||||
QY 5221 TTGAACATTAAGCAATTAACAAAGAGAAAGCCCAATTTATGTTTCAAAATTTAGGGT 5280
DB |||||
QY 2881 TTTAACTTTTGAAGCAAACTTTTATGCTTGTGACCTGACAGACTGTACTCAGAT 2940
DB |||||
QY 5281 TTTAACTTTTGAAGCAAACTTTTATGCTTGTGACCTGACAGACTGTACTCAGAT 5340
DB |||||
QY 2941 TTTGCTATGAGTTAAAGATGATACCAAGCTGTGCTGTAATGATGTTTCTCAGAT 3000
DB |||||
QY 5341 TTTGCTATGAGTTAAAGATGATACCAAGCTGTGCTGTAATGATGTTTCTCAGAT 5400
DB |||||
QY 3001 TTTCTGTGTTGACAGTTTAAATTTAGCAGTCAATACATTTGCAAAAGTAGAATGACCTC 3060
DB |||||
QY 5401 TTTCTGTGTTGACAGTTTAAATTTAGCAGTCAATACATTTGCAAAAGTAGAATGACCTC 5460
DB |||||
QY 3061 ATAAATACCTCTTCAAAATGCTTAAATTCATTTCAACATTAATTTATCTCAGCTTG 3120
DB |||||
QY 5461 ATAAATACCTCTTCAAAATGCTTAAATTCATTTCAACATTAATTTATCTCAGCTTG 5520
DB |||||
QY 3121 AAGCAATTCAGTAGTGCATGGAATCAAGCCTGGGCTACCTGATGCTGTTCTCTTCT 3180
DB |||||
QY 5521 AAGCAATTCAGTAGTGCATGGAATCAAGCCTGGGCTACCTGATGCTGTTCTCTTCT 5580
DB |||||
QY 3181 TTTCTCTTTTAAAGCAATTTTGTCTAAGACAGCTTCTTCAAAACACTTGCTTCTCCTA 3240
DB |||||
QY 5581 TTTCTCTTTTAAAGCAATTTTGTCTAAGACAGCTTCTTCAAAACACTTGCTTCTCCTA 5640
DB |||||
QY 3241 TTTTGTGTTTACTAGTTTAAAGATCAGAGTCACTTTCTTTGAGTCTGCTCATATTTTCT 3300
DB |||||
QY 5641 TTTTGTGTTTACTAGTTTAAAGATCAGAGTCACTTTCTTTGAGTCTGCTCATATTTTCT 5700
DB |||||
QY 3301 TACCTGAACCTTTGCAAGTTTTCAGGTAACTCAGTCAAGAGCTGCTATTTACTCCTC 3360
DB |||||
QY 5701 TACCTGAACCTTTGCAAGTTTTCAGGTAACTCAGTCAAGAGCTGCTATTTACTCCTC 5760
DB |||||
QY 3361 TTAAGAAATTAATAAAAAAAAAAAG 3387
DB |||||
QY 5761 TTAAGAAATTAATAAAAAAAAAAAG 5787
DB |||||

RESULT 9
AAF21117
ID AAF21117 standard; DNA; 15240 BP.
XX
```

AC AAF21117;  
XX 14-MAR-2001 (first entry)  
DB Human low adenosine antisense oligonucleotide related sequence #2684.  
XX  
KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KM human; airway disorder; bronchoconstriction; lung inflammation;  
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KM immunosuppressive; antiallergic; hypotensive; cyostatic;  
KM respiratory obstruction; pulmonary obstruction; impeded respiration;  
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KM cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO20062736-A2.  
XX  
XX 26-OCT-2000.  
XX  
XX 24-MAR-2000; 2000WO-US008020.  
XX  
XX 06-APR-1999; 99US-0127958P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX (NYCE/) NYCE J W.  
XX  
XX Nlyce JW;  
XX  
XX WPI; 2000-679539/66.  
XX  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
XX adenosine receptors during metabolism, useful e.g. for treating cancers  
XX and respiratory obstructions.  
XX  
XX  
XX Disclosure; Page 968-972; 1592pp; English.  
XX  
XX The present invention describes low adenosine (A) content antisense  
XX oligonucleotides and compositions (I) comprising them. In the antisense  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antistimatic, hypotensive and cyostatic activities.  
XX The antisense oligonucleotides and (I) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with  
XX lung/respiratory disorders and malignancies, such as stimulating and  
XX activating peptide factors and transmitters, transcription factors,  
XX immunoglobulins and antibodies, antibody receptors, cytokines and  
XX chemokines, endogenously produced specific and non-specific enzymes,  
XX binding proteins, adhesion molecules and their receptors, cytokine and  
XX chemokine receptors, adenosine receptors, bradykinin receptors, central  
XX nervous system (CNS) and peripheral nervous and non-nervous system  
XX receptors, CNS and peripheral nervous and non-nervous system peptide  
XX transmitters, defensins, growth factors, vasodilative peptides and  
XX receptors, binding proteins and malignancy associated proteins. The  
XX antisense oligonucleotides may be used in this way to treat disorders  
XX including respiratory obstruction (especially pulmonary obstruction  
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
XX surfactant hypoproduction which are associated with a disease or  
XX condition selected from pulmonary vasoconstriction, inflammation,  
XX allergies, asthma, impeded respiration, respiratory distress syndrome  
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,  
XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
XX fragments and antisense oligonucleotides used in the exemplification of  
XX the present invention  
XX  
XX Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 U; 0 Other;  
XX  
XX Query Match 99.8%; Score 3379; DB 3; Length 15240;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GTCCAGAACTCTCTCAGCAGCGCTCTCTTACGCTCCACAGCCAGCGCCCTCAACAGCA 60  
DB 2401 GTCCAGAACTCTCTCAGCAGCGCTCTCTTACGCTCCACAGCCAGCGCCCTCAACAGCA 2460  
QY 61 AAGCTTACCCCGCGCGCGCGCTTCCGCGCGCTGCGATGCTGCGCGCGCTGCTGCT 120  
DB 2461 AAGCTTACCCCGCGCGCGCGCTTCCGCGCGCTGCGATGCTGCGCGCGCTGCTGCT 2520  
QY 121 GTGCGCGCTCTGCGCGCTCAGCCATACAGCAATCTTGTCTTCCACCCATGTCAAA 180  
DB 2521 GTGCGCGCTCTGCGCGCTCAGCCATACAGCAATCTTGTCTTCCACCCATGTCAAA 2580  
QY 181 CCGAGGTGTATGTATGATGTGTGGATTTGACCAATTAAGTGCATGTACCCGACAGG 240  
DB 2581 CCGAGGTGTATGTATGATGTGTGGATTTGACCAATTAAGTGCATGTACCCGACAGG 2640  
QY 241 ATTCTATGAGAAATCTGCTCAACACCGGATTTTGAACAATAATTAATTTCTGAA 300  
DB 2641 ATTCTATGAGAAATCTGCTCAACACCGGATTTTGAACAATAATTAATTTCTGAA 2700  
QY 301 ACCCATTCGAAACACAGTGCATACATCTTACCCACTTCAAGGATTTTGGAACTTGT 360  
DB 2701 ACCCATTCGAAACACAGTGCATACATCTTACCCACTTCAAGGATTTTGGAACTTGT 2760  
QY 361 GAATTAACCTTCCCTCTTCTGGAATGCAATATGATATGTTATGTCATGCAATCACA 420  
DB 2761 GAATTAACCTTCCCTCTTCTGGAATGCAATATGATATGTTATGTCATGCAATCACA 2820  
QY 421 TTGATTAACAGTCCACCACTTACAAATGCTAGTATGCTTCAAAAGCTGGAAGCCTT 480  
DB 2821 TTGATTAACAGTCCACCACTTACAAATGCTAGTATGCTTCAAAAGCTGGAAGCCTT 2880  
QY 481 CTTAACCTCTCTTATTAATTAATGAGCCCTTCTCTGCTGCTGATGATTTGCCAGCTCC 540  
DB 2881 CTTAACCTCTCTTATTAATTAATGAGCCCTTCTCTGCTGCTGATGATTTGCCAGCTCC 2940  
QY 541 CTGGGCTTCAAAAGGTAAAGACAGCTTCTGATTCAAATGATGTTGGAAAAATGCT 600  
DB 2941 CTGGGCTTCAAAAGGTAAAGACAGCTTCTGATTCAAATGATGTTGGAAAAATGCT 3000  
QY 601 TCTAAGAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAAAACATGATGTTGCTTTTGC 660  
DB 3001 TCTAAGAAAGAAAGTTCAATCCCTGATCCCAAGGCTCAAAACATGATGTTGCTTTTGC 3060  
QY 661 CCAGCACTTCAAGCAGCAAGTTTTCAGACAGATCATAGGAGGCGCACTTTCAACCA 720  
DB 3061 CCAGCACTTCAAGCAGCAAGTTTTCAGACAGATCATAGGAGGCGCACTTTCAACCA 3120  
QY 721 CGGGCTGGGCGCAATGGGGTGGAGCTTAATCATATTAGGTTGAACTCTGGCTAGACAGG 780  
DB 3121 CGGGCTGGGCGCAATGGGGTGGAGCTTAATCATATTAGGTTGAACTCTGGCTAGACAGG 3180  
QY 781 TAAATCGGCGCTTTTCAAGGATGAGTAAAAATGAAATATGATTAATGATGAGAGATGA 840  
DB 3181 TAAATCGGCGCTTTTCAAGGATGAGTAAAAATGAAATATGATTAATGATGAGAGATGA 3240  
QY 841 TCTTCCACAGTCAAAAGATTAATCTCAGCAGAGATTAATCTTCTCTCAAGTCCCTGAGGA 900  
DB 3241 TCTTCCACAGTCAAAAGATTAATCTCAGCAGAGATTAATCTTCTCTCAAGTCCCTGAGGA 3300  
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DB 3301 TCTAAGGTTTGTGTGGGCGAGAGTCTTGTGCTGCTGCTGCTGATGATATGTC 3360  
QY 961 CACAATCTGCTGCGGAGAACACACAGAGATATGATGTTGTTAAACAGAGACATCTCTGA 1020  
DB 3361 CACAATCTGCTGCGGAGAACACACAGAGATATGATGTTGTTAAACAGAGACATCTCTGA 3420  
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Db 3421 ATGGGGTGAATGACGCTTCTTCCAGCAACAGGCTAATAGAGAGACATTTAA 3480  
QY 1081 GATTGTGATGGAATTAATGTCACACACTTGAAGGCTATCACTTCAACCTGAATTTGA 1140  
Db 3481 GATTGTGATGGAATTAATGTCACACACTTGAAGGCTATCACTTCAACCTGAATTTGA 3540  
QY 1141 CCCAGACATCACTTTTCAACAAACAAATTCAGTACCAAAATGATTTGCTGTGAATTTAA 1200  
Db 3541 CCCAAACCTACTTTTCAACAAACAAATTCAGTACCAAAATGATTTGCTGTGAATTTAA 3600  
QY 1201 CACCTGTATGACCTGGCAATCCCTCTGCTGACAGCCTTTCAAAATTCAGTACCAAAAT 1260  
Db 3601 CACCTGTATGACCTGGCAATCCCTCTGCTGACAGCCTTTCAAAATTCAGTACCAAAAT 3660  
QY 1261 CAACATCAACAGTTTATCTACACAACTATATTTGCTGGAACAGTAAATTCACCAAT 1320  
Db 3661 CAACATCAACAGTTTATCTACACAACTATATTTGCTGGAACAGTAAATTCACCAAT 3720  
QY 1321 TGTGATCATTTACACAGCAAAATTCCTGGCAGGGTTCCTGCTGAGAAATTTTCAAC 1380  
Db 3721 TGTGATCATTTACACAGCAAAATTCCTGGCAGGGTTCCTGCTGAGAAATTTTCAAC 3780  
QY 1381 CGCAGTACAGAAAGTATACAGGGCTTCGATTCACAGACAGGACGATGAATTCACAGT 1440  
Db 3781 CGCAGTACAGAAAGTATACAGGGCTTCGATTCACAGACAGGACGATGAATTCACAGT 3840  
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Db 3841 TTTTAAATGATACGCAAAAGCTTTATGCTGAAGCCCTATGAAATCATTTGAAGAATTC 3900  
QY 1501 AGGAGAAAAGAAATGTCTGACAGGTTGGAAGCACTATGATGACATGATGCTGTGA 1560  
Db 3901 AGGAGAAAAGAAATGTCTGACAGGTTGGAAGCACTATGATGACATGATGCTGTGA 3960  
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Db 4021 GGTGAAGTTGAGACACCATTCCTCTTGAAGAACTTATGGTATGTTATATGTTCTCC 4080  
QY 1681 TGCTTACTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAATCATCAACACTGC 1740  
Db 4081 TGCTTACTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAATCATCAACACTGC 4140  
QY 1741 CTCAATTCAGTCTCTCATCTGTCATTAAGTGAAGGGCTGCCCTTACTTACTCAAGT 1800  
Db 4141 CTCAATTCAGTCTCTCATCTGTCATTAAGTGAAGGGCTGCCCTTACTTACTCAAGT 4200  
QY 1801 TCCGATTCAGAGCTCATTTAAACAGTCAACCATCAATGCAAGTCTTCCGCTCCGAGT 1860  
Db 4201 TCCGATTCAGAGCTCATTTAAACAGTCAACCATCAATGCAAGTCTTCCGCTCCGAGT 4260  
QY 1861 AGATGATATCAATCCCAAGTACATCTTAAAGAAAGGCTGCACTGAACGTGAAGTCTAA 1920  
Db 4261 AGATGATATCAATCCCAAGTACATCTTAAAGAAAGGCTGCACTGAACGTGAAGTCTAA 4320  
QY 1921 TGAATCATATTTATTTATTAATGACCATGTCATTAATTTATTTATTAATTAATTTT 1980  
Db 4321 TGAATCATATTTATTTATTAATGACCATGTCATTAATTTATTTATTAATTAATTTT 4380  
QY 1981 ATATTAACCTCTTATGTTACTTAACATCTTCTGTAACAGAAAGTCACTACTCTGTCGG 2040  
Db 4381 ATATTAACCTCTTATGTTACTTAACATCTTCTGTAACAGAAAGTCACTACTCTGTCGG 4440  
QY 2041 GAGAAAGAGTCAATCTTGAAGAACTTTATGCTATCACTCTTAAGATTTTGTGTGC 2100  
Db 4441 GAGAAAGAGTCAATCTTGAAGAACTTTATGCTATCACTCTTAAGATTTTGTGTGC 4500  
QY 2101 TGTAAATTTGAAAAAGATTTTATCTGTTTATTAACAGAGAGAAATGATTTGA 2160  
Db 4501 TGTAAATTTGAAAAAGATTTTATCTGTTTATTAACAGAGAGAAATGATTTGA 4560

QY 2161 GCTCTTTTACTGAAATTTCACTTATATTAATGAAGAAAGTAAAGTGTGTAATAC 2220  
Db 4561 GCTCTTTTACTGAAATTTCACTTATATTAATGAAGAAAGTAAAGTGTGTAATAC 4620  
QY 2221 TTAACACTATCAACAAGATGCAAAATGCTGAAGTTTTCACGTGAGTGTCCAT 2280  
Db 4621 TTAACACTATCAACAAGATGCAAAATGCTGAAGTTTTCACGTGAGTGTCCAT 4680  
QY 2281 GCAATTCATGATGATTAAGATTAATGTTGAATTTTAAAGTACTTTTGGGTA 2340  
Db 4681 GCAATTCATGATGATTAAGATTAATGTTGAATTTTAAAGTACTTTTGGGTA 4740  
QY 2341 TTTTCTGCTCAACAAAGAAACAGGATCACTGCTTTTAAATGAATTTAAATGA 2400  
Db 4741 TTTTCTGCTCAACAAAGAAACAGGATCACTGCTTTTAAATGAATTTAAATGA 4800  
QY 2401 CATTACAGATTAATTCATGCTCACTTTTAAATAGCAATGAACAAATTTGAATTT 2460  
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Db 4861 TCTAAATTCATAGGGTGAATCACCTGTAAAGCTTGTGATTTCTTAAAGTTATTA 4920  
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Db 4981 TTACTCAATTTGCTGTTAAATTTATTAATGATGATGCTCTTTTACCAAGATTA 5040  
QY 2641 AACCTTTTATGCTGATTTAAATCTCTTTTAAATCAAAATGCCAAATTTAAAG 2700  
Db 5041 AACCTTTTATGCTGATTTAAATCTCTTTTAAATCAAAATGCCAAATTTAAAG 5100  
QY 2701 TGGTGAAGCACTGCAAGTATTAATCAAAATTAATCTGTTGATTAATTCAGAT 2760  
Db 5101 TGGTGAAGCACTGCAAGTATTAATCAAAATTAATCTGTTGATTAATTCAGAT 5160  
QY 2761 CTGTTTATGAGCTGTGAATGAATTAATTAATGAAGTGTCTTTTACCAAGGAT 2820  
Db 5161 CTGTTTATGAGCTGTGAATGAATTAATTAATGAAGTGTCTTTTACCAAGGAT 5220  
QY 2821 TTGAACATTAAGCAATTAACAAAGAGAAAGCCCAATTTATGTTTCAATTTAGG 2880  
Db 5221 TTGAACATTAAGCAATTAACAAAGAGAAAGCCCAATTTATGTTTCAATTTAGG 5280  
QY 2881 TTAACCTTTTGAAGCAACCTTTTATGCTTGTGCACTGCAAGTCTGCTAGAT 2940  
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QY 2941 TTGCTATGAGGTTAATGAAGTACCAAGCTGTCTTGAATTAATGTTTCTAGAT 3000  
Db 5341 TTGCTATGAGGTTAATGAAGTACCAAGCTGTCTTGAATTAATGTTTCTAGAT 5400  
QY 3001 TTTCTGTGTAAGCTTTAATTTAGAGCTCAATTCATTTGCAAAAGTGAAGTACCTC 3060  
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QY 3061 ATAAATTAACCTCTTCAAAATGCTTAAATTAATTAATTAATTAATTAATTAAT 3120  
Db 5461 ATAAATTAACCTCTTCAAAATGCTTAAATTAATTAATTAATTAATTAATTAAT 5520  
QY 3121 AAGCAATTAAGTGAAGTGAATGAATCAAGCTGTGCTAGCTGATGCTGCTTCT 3180  
Db 5521 AAGCAATTAAGTGAAGTGAATGAATCAAGCTGTGCTAGCTGATGCTGCTTCT 5580  
QY 3181 TTTCTTCTTTTACCAATTTTGTGAAGACAGTCTTCTCAAACTTGTGTTCTCTA 3240  
Db 5581 TTTCTTCTTTTACCAATTTTGTGAAGACAGTCTTCTCAAACTTGTGTTCTCTA 5640

CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 15240 BP; 4672 A; 2944 C; 2804 G; 4820 T; 0 U; 0 Other;  
 Query Match 99.8%; Score 3379; DB 7; Length 15240;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

3241 TTTGTTTACAGTTTAAAGTCAGAGTCCTTTCTTGAGCTGCTATATTTCT 3300  
 DB TTTGTTTACAGTTTAAAGTCAGAGTCCTTTCTTGAGCTGCTATATTTCT 5700

QY 3301 TACCTGAACCTTTTGACAGTTTTCAGAGTAAACCTGACGACTGCTATTAGCTCTC 3360  
 DB TACCTGAACCTTTTGACAGTTTTCAGAGTAAACCTGACGACTGCTATTAGCTCTC 5760

QY 3361 TTAAGAAAGTTTAAAAAAG 3387  
 DB TTAAGAAAGTTTAAAAAAG 5787

RESULT 10  
 ID ABZ96811 standard; DNA; 15240 BP.  
 XX ABZ96811;  
 AC  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human nucleic acid sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasmatic; hypotensive; immunosuppressive; cytosolic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahbuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 12053; 872bp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasmatic, hypotensive,  
 CC immunosuppressive, and cytosolic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO

1 GTCCAGGAACCTCCAGAGAGGCTCTTCAGCTCCACAGCCACAGCCCTCAGACACA 60  
 DB GTCCAGGAACCTCCAGAGAGGCTCTTCAGCTCCACAGCCACAGCCCTCAGACACA 2460

QY 61 AAGCCTACCCCGCGCGCGCCCTGCGCGCGCTGCGCGCGCTGCGCGCTGCT 120  
 DB AAGCCTACCCCGCGCGCGCCCTGCGCGCGCTGCGCGCGCTGCGCGCTGCT 2520

QY 121 GTGCGCGGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCT 180  
 DB GTGCGCGGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCT 2580

QY 181 CGGAGGTAT 240  
 DB CGGAGGTAT 2640

QY 241 ATTCTATGAGAAAACCTGCTCAACACCGGAAATTTTGAAGAATTAATTTCTGAA 300  
 DB ATTCTATGAGAAAACCTGCTCAACACCGGAAATTTTGAAGAATTAATTTCTGAA 2700

QY 301 ACCCACTCCAAAACAGAGTGCATCATCTTACCACCTTCAAGGATTTTGGAAAGTTGT 360  
 DB ACCCACTCCAAAACAGAGTGCATCATCTTACCACCTTCAAGGATTTTGGAAAGTTGT 2760

QY 361 GAATTAACATTCCTCTCTTCCGAAATGCAATATATATATATATATATATATAT 420  
 DB GAATTAACATTCCTCTCTTCCGAAATGCAATATATATATATATATATATAT 2820

QY 2761 GAATTAACATTCCTCTCTTCCGAAATGCAATATATATATATATATATATAT 2820  
 DB GAATTAACATTCCTCTCTTCCGAAATGCAATATATATATATATATATATAT 2880

QY 421 TTTGATTAACAGTCCACCACTTACATATGCTGATGCTGCTGCTGCTGCTGCT 480  
 DB TTTGATTAACAGTCCACCACTTACATATGCTGATGCTGCTGCTGCTGCTGCT 2880

QY 481 CTCTTAACCT 540  
 DB CTCTTAACCT 2940

QY 2881 CTCTTAACCT 2940  
 DB CTCTTAACCT 3000

QY 541 CTTGGGTGTCAAAAGGTAAAGAGCTTCTGATTCATATGATGATGATGATGATGAT 600  
 DB CTTGGGTGTCAAAAGGTAAAGAGCTTCTGATTCATATGATGATGATGATGATGAT 3000

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QY 601 TCTAAGAAAGAAATTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 660  
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QY 3001 TCTAAGAAAGAAATTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 3060  
 DB TCTAAGAAAGAAATTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 3120

QY 661 CCAGCACTTCACGCAACGATTTTCAAGACAGATCATTAAGGAGGCGGAGCTTACCA 720  
 DB CCAGCACTTCACGCAACGATTTTCAAGACAGATCATTAAGGAGGCGGAGCTTACCA 3120

QY 3061 CCAGCACTTCACGCAACGATTTTCAAGACAGATCATTAAGGAGGCGGAGCTTACCA 3120  
 DB CCAGCACTTCACGCAACGATTTTCAAGACAGATCATTAAGGAGGCGGAGCTTACCA 3180

QY 721 CGGGCTGGGCGCATGGGGGAGATTAATCATATTTAATCGGTGAATCTGGCTAGACAGCG 3180  
 DB CGGGCTGGGCGCATGGGGGAGATTAATCATATTTAATCGGTGAATCTGGCTAGACAGCG 3240

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QY 3181 TAAACTGCGCTTTCAAGAGATGAAAAATGAATATATATATATATATATATATAT 3240  
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QY 841 TCCTCCACAGTCAAGATTAATCTCAAGCAAGATTAATCTCAAGTCCCTGAGCA 900  
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QY 3241 TCCTCCACAGTCAAGATTAATCTCAAGCAAGATTAATCTCAAGTCCCTGAGCA 900  
 DB TCCTCCACAGTCAAGATTAATCTCAAGCAAGATTAATCTCAAGTCCCTGAGCA 3360

QY 901 TCTAAGGTTTGTGTTGAGGAGAGAGGATTTTGTGTTGTTGTTGTTGTTGTTGTT 960  
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QY 3301 TCTAAGGTTTGTGTTGAGGAGAGAGGATTTTGTGTTGTTGTTGTTGTTGTTGTT 3360  
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QY 961 CACAAATCTGGCTGGGGAACACAAACAGAGTATGATGATGATGATGATGATGATGAT 1020

Db 3361 CACAATCTGGCTGAGGAAACACAGAGATATGCGATGCTTAAACAGAGACCTCTGA 3420  
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 Db 3481 GATTGTGATTGAAGATTATGTGSCAACACTTGAGTGGCTATCACTTCAAACTGAAATTGA 3540  
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 Db 3781 CGCAGTACAGAAAGTATCATCAGGCTTCCATTGACACAGAGCAGGAGATGAATATCACATC 3840  
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 Db 4021 GGTAGAGTGGAGACCACTTCTCTTGAAGAACTTATGGGTAAATGTTATATGTTCTCC 4080  
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 Db 4081 TGCCCTACTGSAAGCCACACACTTTTGTGAGAAAGTGGGTTTTCAAATCATCAACACCTGC 4140  
 Qy 1741 CTCAATTCACTCTCTCATCTGCAATTAACGTGAAGGGGTGCTCCCTTACTTCAATCAAGT 1800  
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 Qy 1861 AGAGATATCAATCCACAGTACCTAATAAGAAAGCTGCACTGAACGTGAAAGTCTAA 1920  
 Db 4261 AGAGATATCAATCCACAGTACCTAATAAGAAAGCTGCACTGAACGTGAAAGTCTAA 4320  
 Qy 1921 TGATCATATTTATTTATTTATATGAAACATGCTATTAATTAATTTATTAATATTTT 1980  
 Db 4321 TGATCATATTTATTTATTTATATGAAACATGCTATTAATTAATTTATTAATATTTT 4380  
 Qy 1981 ATATTTAACTCTTATGTTACTTAAACATCTTCTGTAAACAGAAAGTCACTCTCTGTGCG 2040  
 Db 4381 ATATTTAACTCTTATGTTACTTAAACATCTTCTGTAAACAGAAAGTCACTCTCTGTGCG 4440  
 Qy 2041 GAGAAGAGTCACTACTTGTGAAGACTTTTATGTCACTACTTAAAGATTTTGTGTGTC 2100

Db 4441 GAGAAGAGTCACTACTTGTGAGACTTTTATATGTCACTACTTAAAGATTTTGTGTGTC 4500  
 Qy 2101 TGTATGTTGGAAAAAGTTTATATCTGTTTATTAACCGAGAGAAATGAGTTTGA 2160  
 Db 4501 TGTATGTTGGAAAAAGTTTATATCTGTTTATTAACCGAGAGAAATGAGTTTGA 4560  
 Qy 2161 CGCTTTTATCTGTAATTTCACTTATTAATTAAGAGAAAGTAAAGTGTGGAATAC 2220  
 Db 4561 CGCTTTTATCTGTAATTTCACTTATTAATTAAGAGAAAGTAAAGTGTGGAATAC 4620  
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 Db 4741 TTTTCTGTCATCAACAAACAGGATCAGTGCATTAATTAATGAATATTAAATTTGA 4800  
 Qy 2401 CATTAACAATTAATTCATGCTACTTTTAAATCAACAATGAACAAATTAATTTGAAT 2460  
 Db 4801 CATTAACAATTAATTCATGCTACTTTTAAATCAACAATGAACAAATTAATTTGAAT 4860  
 Qy 2461 TCTAAATTCATAGGGTGAATCACCTGTAAGCTGTGTAATTTCTTAAGTTATTA 2520  
 Db 4861 TCTAAATTCATAGGGTGAATCACCTGTAAGCTGTGTAATTTCTTAAGTTATTA 4920  
 Qy 2521 CTGTACATTAACAAAGAGCTGTGCTGATTTAAATCTGTAATTCAGATGAATTT 2580  
 Db 4921 CTGTACATTAACAAAGAGCTGTGCTGATTTAAATCTGTAATTCAGATGAATTT 4980  
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 Db 4981 TTACTACATTCGTTGTTAAATTTTAAATGATGATGTTCTTTTACCAAGAGTATA 5040  
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 Db 5041 AACCTTTTATGAGTGAAGCTTAAACCTTCTTAAATCAAAAGCCAAATTTATTAAG 5100  
 Qy 2701 TGTGAGGCCACTCAGTGTATCTCAAAATTAAGAAATCTGTTGAGATTTCCAGAT 2760  
 Db 5101 TGTGAGGCCACTCAGTGTATCTCAAAATTAAGAAATCTGTTGAGATTTCCAGAT 5160  
 Qy 2761 CTGTTTATATGCTGTGTAACATGTAATAACCCATAACCCCGCAAAAGGGGTCTTACC 2820  
 Db 5161 CTGTTTATATGCTGTGTAACATGTAATAACCCATAACCCCGCAAAAGGGGTCTTACC 5220  
 Qy 2821 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGCTTCCAAATTTAGGGT 2880  
 Db 5221 TTGAACATTAAGCAATTAACCAAGAGAAAGCCCAATTAATGCTTCCAAATTTAGGGT 5280  
 Qy 2881 TTAAACTTTTGAAGCAACTTTTATAGCTTGTGCACTGACAGCTGTACTCAGAT 2940  
 Db 5281 TTAAACTTTTGAAGCAACTTTTATAGCTTGTGCACTGACAGCTGTACTCAGAT 5340  
 Qy 2941 TTTGCTATGAGGTTAAAGAGTACCAAGCTGTGCTTGAATAGATATGTTTCTCAGAT 3000  
 Db 5341 TTTGCTATGAGGTTAAAGAGTACCAAGCTGTGCTTGAATAGATATGTTTCTCAGAT 5400  
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 Db 5401 TTTCTGTGTGACAGTTAATTTATAGCAGCTATCAATGCAAAAGAGACATGAGCTC 5460  
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 Db 5461 ATAAATTAACCTTTCAAAATGCTTAAATTCATTTCAACATTAATTTATCTCAGCTTG 5520  
 Qy 3121 AAGCCAATCAGTAGTGTGCAATGGAATCAAGCTGTGCTACTGTGATGCTGTTTCT 3180  
 Db 5521 AAGCCAATCAGTAGTGTGCAATGGAATCAAGCTGTGCTACTGTGATGCTGTTTCT 5580





Db 938 TCTACGGTTGCTGTGCGGACAGAGGCTCTTGTGCTGCGCTGCTGATATGATGTC 997  
Qy 961 CACAAATCGGCTGCGGAAACACAAAGAGTATGTGATGTCTTAAACAGAGCATCTGGA 1020  
Db 998 CACAATCTGGCTGCGGAAACACAAAGAGTATGTGATGTCTTAAACAGAGCATCTGGA 1057  
Qy 1021 AAGGGGTGATGAGCATGTGTCTTCAAGACAGCGCTAATCTGATAGAGAGACTATTA 1080  
Db 1058 AAGGGGTGATGAGCATGTGTCTTCAAGACAGCGCTAATCTGATAGAGAGACTATTA 1117  
Qy 1081 GATTGTGATGAGTAAATGTCGAACCTTGAGTGGCTATGACTTCAAACTGAATTGGA 1140  
Db 1118 GATTGTGATGAGTAAATGTCGAACCTTGAGTGGCTATGACTTCAAACTGAATTGGA 1177  
Qy 1141 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGATATGCTGCTGAATTA 1200  
Db 1178 CCCAGAACTACTTTTCAACAAACAAATTCAGTACCAAAATGATATGCTGCTGAATTA 1237  
Qy 1201 CACCTCTATCACTGGGCATTCCTCTGCTGACACCTTTCAAATTCATGACCAAAATA 1260  
Db 1238 CACCTCTATCACTGGGCATTCCTCTGCTGACACCTTTCAAATTCATGACCAAAATA 1297  
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Qy 1381 CGCAGTACAGAAAGTATCAAGGCTTCATTTGACCAAGACAGCGAGATGAATAACCACTC 1440  
Db 1418 CGCAGTACAGAAAGTATCAAGGCTTCATTTGACCAAGACAGCGAGATGAATAACCACTC 1477  
Qy 1441 TTTTAATGATGACGCAAAAGCTTATGCTGAAGCCCTAATGATATTTGAAGAACTTAC 1500  
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Qy 1501 AGGAGAAAAGGAAATGCTGACAGATTTGAAGACACTGTATGTCATCATGACGCTGGA 1560  
Db 1538 AGGAGAAAAGGAAATGCTGACAGATTTGAAGACACTGTATGTCATCATGACGCTGGA 1597  
Qy 1561 GCTGTATCTGCTCTTCTGTGTAAGAAAGCCCTGCGCAAGATSCCATCTTTGGTGAACCAT 1620  
Db 1598 GCTGTATCTGCTCTTCTGTGTAAGAAAGCCCTGCGCAAGATSCCATCTTTGGTGAACCAT 1657  
Qy 1621 GGTAGAAGTTGAGACACCATCTGCTTGAAGAACTATGGGTAAATGTTATGTTCTCC 1680  
Db 1658 GGTAGAAGTTGAGACACCATCTGCTTGAAGAAAGCTTATGGGTAAATGTTATGTTCTCC 1717  
Qy 1681 TGCCTACTGGAAGCCAAAGCACTTTTGGTGAAGAGTGGTTTCAAAATCATCAACACCTGC 1740  
Db 1718 TGCCTACTGGAAGCCAAAGCACTTTTGGTGAAGAGTGGTTTCAAAATCATCAACACCTGC 1777  
Qy 1741 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGCTGTCCCTTTAATTCAATCAGTGT 1800  
Db 1778 CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGCTGTCCCTTTAATTCAATCAGTGT 1837  
Qy 1801 TCCAGATCCAGAGCTGCTTAAACAGTCAACATCAATGCAAGTCTTCCGCTCCGACT 1860  
Db 1838 TCCAGATCCAGAGCTGCTTAAACAGTCAACATCAATGCAAGTCTTCCGCTCCGACT 1897  
Qy 1861 AGATGATATCAATCCACAGTACTACTAATAAGAAAGCGTCACTGAACTGTAGAAAGTCTAA 1920  
Db 1898 AGATGATATCAATCCACAGTACTACTAATAAGAAAGCGTCACTGAAAGTCTAA 1957  
Qy 1921 TGAATCATTTATTTATTTATTAATGAACCATGTCTAATTAATTAATTAATTAATTAATTT 1980  
Db 1958 TGAATCATTTATTTATTTATTAATGAACCATGTCTAATTAATTAATTAATTAATTAATTT 2017  
Qy 1981 ATATTAACCTCCTATGTACTTAACATCTTCTGTACAGAAAGTCACTACTCTGTTGCG 2040

Db 2018 ATATTAACCTCCTATGTACTTAACATCTTCTGTACAGAAAGTCACTACTCTGTTGCG 2077  
Qy 2041 GAGAAAGAGTCATCTTGTGAAGCTTTTATGTCACTAATCTTAAAGATTTGCTGTGCG 2100  
Db 2078 GAGAAAGAGTCATCTTGTGAAGCTTTTATGTCACTAATCTTAAAGATTTTGTGCTGTGCG 2137  
Qy 2101 TGTAAAGTTTGAAGAAACAGTTTATGCTGTTTAAACAGAGAAATGAGTTTGA 2160  
Db 2138 TGTAAAGTTTGAAGAAACAGTTTATGCTGTTTAAACAGAGAAATGAGTTTGA 2197  
Qy 2161 GCTCTTTTACTGTAATTTCAACTAATTAATTAAGACGAAAGTAAAGATGTTGAATAC 2220  
Db 2198 GCTCTTTTACTGTAATTTCAACTAATTAATTAAGACGAAAGTAAAGATGTTGAATAC 2257  
Qy 2221 TTAAACACTATCACAAGATGCAAAATGCTGAAGTTTTCACCTGTGAGTTCCAAT 2280  
Db 2258 TTAAACACTATCACAAGATGCAAAATGCTGAAGTTTTCACCTGTGAGTTCCAAT 2317  
Qy 2281 GCATCTTCATGATGATTAAGAGTAAATGTTGAATTTTAAAGTACTTTGGGTA 2340  
Db 2318 GCATCTTCATGATGATTAAGAGTAAATGTTGAATTTTAAAGTACTTTGGGTA 2377  
Qy 2341 TTTTCTGTCTATCAAAAC-AAAAAGATATCAGTGCATTTTAATGAATATTTAAATGAG 2399  
Db 2378 TTTTCTGTCTATCAAAACAAAAAGATATCAGTGCATTTTAATGAATATTTAAATGAG 2437  
Qy 2400 ACATTTACAGTAATTTCAATGCTCTACTTTTAAATTCAGCATGAAACATAATTTGAAT 2459  
Db 2438 ACATTTACAGTAATTTCAATGCTCTACTTTTAAATTCAGCATGAAACATAATTTGAAT 2497  
Qy 2460 TTCTAAATTCATAGGATGAATCACTGTAAGAAAGCTGTTGATTTCTTAAAGTAAATTA 2519  
Db 2498 TTCTAAATTCATAGGATGAATCACTGTAAGAAAGCTGTTGATTTCTTAAAGTAAATTA 2557  
Qy 2520 ACTGTACATATACCAAAAGAGCTGTCTGGAATTAATCTGTAATTCAGATGAAT 2579  
Db 2558 ACTGTACATATACCAAAAGAGCTGTCTGGAATTAATCTGTAATTCAGATGAAT 2617  
Qy 2580 TTTACTACAAATGCTGTTTAAATATTTTATTAAGTATGTTCTTTTACCAAGAGTAT 2639  
Db 2618 TTTACTACAAATGCTGTTTAAATATTTTATTAAGTATGTTCTTTTACCAAGAGTAT 2677  
Qy 2640 AAACCTTTTATGATGCTGTTTAAACCTTCTTTAATCAAAATGCAAAATTTATTAAG 2699  
Db 2678 AAACCTTTTATGATGCTGTTTAAACCTTCTTTAATCAAAATGCAAAATTTATTAAG 2737  
Qy 2700 GTGTGAGACCACTGCAAGTATCTCAAAATGAAGATATCTGTGAGATTTCCAGAA 2759  
Db 2738 GTGTGAGACCACTGCAAGTATCTCAAAATGAAGATATTTGTGAGATTTCCAGAA 2797  
Qy 2760 TCTGTTATATGCTGTTAATCATGTAAACCCCATTAACCCCGCAAAAGGGTCTTACC 2819  
Db 2798 TCTGTTATATGCTGTTAATCATGTAAACCTTATATAGC-----AAAAGGGTCTTACC 2850  
Qy 2820 CTTGAACATTAAGCAATTAACCAAGGAGAAAGCCCAATTAATGTTCCAAATTTTGGG 2879  
Db 2851 TTTTAA-----AAATGAACATTAACCAAGGAGAAAGCCCAATTAATGTTCCAAATTTTGG 2901  
Qy 2880 TTTTAACTTTTGAAGCAAACTTTTATGCTTGTGACCTGCACTGCAAGCTGTGATCAGAA 2939  
Db 2902 GTTTTAACTTTTGAAGCAAACTTTTATGCTTGTGACCTGCAAGCTGTGATCAGAA 2961  
Qy 2940 TTTTGTATGAGGTTTAAAGATTAAGCAAGCTGTGCTGGAATTAAGATATGTTTCTCAGA 2999  
Db 2962 TTTTGTATGAGGTTTAAAGATTAAGCAAGCTGTGCTGGAATTAAGATATGTTTCTCAGA 3021  
Qy 3000 TTTTCTGTGTATAGTTTATTTAGAGTCAATATCATCTGCAAAAGTGAATGACT 3059  
Db 3022 TTTTCTGTGTATAGTTTATTTAGAGTCAATATCATCTGCAAAAGTGAATGACT 3081  
Qy 3060 CATAAATATCTCTTCAAAATGCTTAAATTCATTTACATTAATTTATCTCAGTCTT 3119  
Db 3082 CATAAATATCTCTTCAAAATGCTTAAATTCATTTACATTAATTTATCTCAGTCTT 3141





QY	1991	ATATTAACTCCCTTAATGTTACTTAAACAATCTCTGTAAACAAGATCAGTACTCTGTGCG	2040
Db	2018	ATATTAACTCCCTTAATGTTACTTAAACATCTCTGTAAACAAGATCAGTACTCTGTGCG	2077
QY	2041	GAGAAAGAGATCACTTGTGAAGACTTTATGTCACTACTCTAAAGCTTTTGGCTGTGC	2100
Db	2078	GAGAAAGAGATCACTTGTGAAGACTTTATGTCACTACTCTAAAGATTTTGGCTGTGC	2137
QY	2101	TGTTAAGTTGGAAAAACAGTTTATTTCTGTTTATTAACACAGAGAGATAGTTTTGA	2166
Db	2138	TGTTAAGTTGGAAAAACAGTTTATTTCTGTTTATTAACACAGAGAGAAATAGTTTTGA	2197
QY	2161	CGTCTTTTACTTGAATTTCACTTAATATTAAAGACAAAGTAAGATGTTGAATAC	2220
Db	2198	CGTCTTTTACTTGAATTTCACTTAATATTAAAGACAAAGTAAGATGTTGAATAC	2257
QY	2221	TTAAACACTATCAAGATGCGAAATGCGTAAAGTTTTCACGTGCGATGTTCCAT	2280
Db	2258	TTAAACACTATCAAGATGCGAAATGCGTAAAGTTTTCACGTGCGATGTTCCAT	2317
QY	2281	GCATCTTCCATGATGCAATTAGAAATCAATATGTTGAATTTTAAAGTACTTTGGGTA	2340
Db	2318	GCATCTTCCATGATGCAATTAGAAATCAATATGTTGAATTTTAAAGTACTTTGGGTA	2377
QY	2341	TTTTTCTGTCTCAAC-AACAAAGGATCATGTCATATTATTAATGAATTTTAATTAG	2399
Db	2378	TTTTTCTGTCTCAACAAACAAACGAGATCATGTCATATTATTAATGAATTTTAATTAG	2437
QY	2400	ACATTACAGATTAATTCAATGCTCACTTTTAAATCGACATGAACAAATAATTGTAAT	2459
Db	2438	ACATTACAGATTAATTCAATGCTCACTTTTAAATCGACATGAACAAATAATTGTAAT	2497
QY	2460	TTCTAAATCACTAGGGTAGATCACTGTAAACCTTGTTGATTTCTTAAAGTTATTTAA	2519
Db	2498	TTCTAAATCACTAGGGTAGATCACTGTAAACCTTGTTGATTTCTTAAAGTTATTTAA	2557
QY	2520	ACTTGATCATTAACCAAAAAAGAGCTGCTTGATTTAAATCTGTAAATCAGATGAAT	2579
Db	2558	ACTTGATCATTAACCAAAAAAGAGAGCTGCTTGATTTAAATCTGTAAATCAGATGAAT	2617
QY	2580	TTTACTCAATGCTGTTTAAATATTTTAAAGTAGTGTTCTTTCACCAAGATAT	2639
Db	2618	TTTACTCAATGCTGTTTAAATATTTTAAAGTAGTGTTCTTTCACCAAGATAT	2677
QY	2640	AAACCTTTTAAAGTGAAGCTGTAAACCTTCCTTTTAAATCAAAATGCGAAATTTATTAAG	2699
Db	2678	AAACCTTTTAAAGTGAAGCTGTAAACCTTCCTTTTAAATCAAAATGCGAAATTTATTAAG	2737
QY	2700	GTGGTGAAGCACATGCAAGTGTATCTCTAAATTAAGAAATATCTGTGAGATTTCCGAA	2759
Db	2738	GTGGTGAAGCACATGCAAGTGTATCTCTAAATTAAGAAATATTTGTTGAGATTTCCGAA	2797
QY	2760	TCTGTTAATATGCTGTGTTAATCATGTAAAAACCCCATATACCCCGCAAAAGGGGCTTACC	2819
Db	2798	TTTGTTTATATAGCTGTGTTAATCATGTAAATCTATATAGC-----AAAAGGCTTACC	2850
QY	2820	CTTGACATTAAGCAATATACCAAGAGAAAGGCCAAATTAATGTTCCAAATTTTAGGG	2879
Db	2851	TTTAA-----AATATGCAATTAACAAAGAAAGAAACCAATTAATGTTCCAAATTTAG	2901
QY	2880	TTTAAACTTTTGAAGCAAACTTTTTTTAAAGCTGTGCACTGCAAGCTGTGTAATCTAGA	2939
Db	2902	GTTTTAACTTTTGAAGCAAACTTTTTTTAAAGCTGTGCACTGCAAGCTGTGTAATCTAGA	2961
QY	2940	TTTTGCATAGAGTTAATGAAGTACCAAGGCTGTGTAATGAAGATGTTTCTAGA	2999
Db	2962	TTTTGCATAGAGTTAATGAAGTACCAAGGCTGTGTAATGAAGATGTTTCTAGA	3021
QY	3000	TTTTTCTGTGATCAGTTTAATTTAGCAATCATATATCATTTGCAAAAGTAGCAATGACT	3059
Db	3022	TTTTTCTGTGATCAGTTTAATTTAGCAATCATATATCATTTGCAAAAGTAGCAATGACT	3081



Db 938 TCTACGGTTTCTGTGGGCGAGAGGCTCTTGGTCTGGGCTGGTGTGATGATGATGCG 997  
QY 961 CACAAATCGGCTCGCGGAAACAACAAGATATGATGATGCTTAAACAGAGACTCTGA 1020  
Db 998 CACAATCGGCTCGCGGAAACAACAAGATATGATGATGCTTAAACAGAGACTCTGA 1057  
QY 1021 ATGGGCTGATGACGCTGTTCTCAGACAAGAGCTTAATCTGATAGAGAGACTATTAA 1080  
Db 1058 ATGGGCTGATGACGCTGTTCTCAGACAAGAGCTTAATCTGATAGAGAGACTATTAA 1117  
QY 1081 GATGTGATGATGAAGTTATNGSCACCTTGATGAGGCTATCACTTCAAACTGAAATTGA 1140  
Db 1118 GATGTGATGATGAAGTTATNGSCACCTTGATGAGGCTATCACTTCAAACTGAAATTGA 1177  
QY 1141 CCCAGAACTACTTTTCAACAAACAATTCAGTACCAAAATGATATGCTGCTGGAATTAA 1200  
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Db 1238 CACCTCTATCACTGGCATCCCTCTTCTGCTGACACCTTCAAAATTCAGTACCAAAATA 1297  
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Db 1358 TGTGAAATCATTCACACAGCAAAATTTGCTGAGAGGTTGCTGTGGTAGAATGTTCCACC 1417  
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Db 1538 AGGAGAAAGGAAATGCTGACAGAGTTGGAAGCACTCTATGCTGACATCGATGCTGGA 1597  
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Db 1598 GCTGATTCCTGCCCTTCTGAGTAAAGAGCCTCGGACAGATCCATCTTTGGTGAACCAT 1657  
QY 1621 GGTAAGAGTTGGAACACCATCTCTCTGAAAGAGCTTATGGGTATGTTATGTTCTCC 1680  
Db 1658 GGTAAGAGTTGGAACACCATCTCTCTGAAAGAGCTTATGGGTATGTTATGTTCTCC 1717  
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Db 1718 TGCTTACTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAAAATCATCAACACTGC 1777  
QY 1741 CTCAATTCAGTCTCTCATCTGCAATAAGTGAAGGCTGTCCCTTTCATTCAGTGT 1800  
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QY 1861 AGATGATATCAATCCACAGTACTACTTAAAGAAAGAGTGCATGACCTGTAAGAGTCTAA 1920  
Db 1898 AGATGATATCAATCCACAGTACTACTTAAAGAAAGAGTGCATGACCTGTAAGAGTCTAA 1957  
QY 1921 TGATCATATTTATTTATTTATATGAACCATGCTATTATTAATTTATTAATTAATTT 1980  
Db 1958 TGATCATATTTATTTATTTATATGAACCATGCTATTATTAATTTATTAATTAATTT 2017  
QY 1981 ATATTAACCTCTATGCTACTTAACATCTTCTGTACAGAAAGCACTACCTCGTTGGC 2040

Db 2018 ATATTAACCTCTCTATGCTACTTAACATCTTCTGTACAGAAAGCACTACCTCGTTGGC 2077  
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QY 2161 GCTCTTTTATCTTGAATTTCACTTAATTAATAAGACGAAAGTAAAGATGTTGAATAC 2220  
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Db 2618 TTTACTPACATGCTGTGTAAATAATTTTAATGATGATGTTTCTTTTACCAAGAGAT 2677  
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Db 3082 CATPAAATACCTCTTCAAAAATGCTTAAATCACTTCAACATTAATTTATCTCAGCTT 3141



QY 841 TCCTCCACAGTCAAGAGTACTCAGCAGAGATGATCTACCTCTCTCAAGTCCCTGAGCA 900  
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Search completed: April 24, 2004, 07:47:37  
Job time : 1231 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 07:25:46 ; Search time 223 Seconds  
(without alignments)  
8428.783 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387  
Sequence: 1 GTCCAGGAACTCTCAGCAG.....GATTAAAAAAAAAAAAAAG 3387

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	3375.8	99.7	3387	2	US-08-627-254C-29
4	3374.2	99.6	3387	3	US-08-930-589A-19
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6	1803.2	53.2	1834	1	US-08-487-753-3
7	1803.2	53.2	1834	1	US-08-487-753-14
8	1803.2	53.2	1834	2	US-08-480-065-3
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12	1803.2	53.2	1834	5	PCT-US93-09167-3
13	1621.6	47.9	3509	4	US-09-919-060-4
14	1621.6	47.9	3509	4	US-09-919-060-6
15	1525.8	45.0	3986	2	US-08-627-254C-27
16	1476.6	43.6	1812	4	US-09-919-060-7
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28	703.6	20.8	1899	4	US-09-919-060-15	Sequence 15, Appl
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31	703.6	20.8	2693	4	US-09-919-060-14	Sequence 14, Appl
32	653.6	19.3	1920	3	US-08-459-493-2	Sequence 2, Appl
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## ALIGNMENTS

RESULT 1  
US-08-064-271-11  
; Sequence 11, Application US/08064271  
; Patent No. 5543297  
; GENERAL INFORMATION:  
; APPLICANT: Kennedy, Brian P.  
; APPLICANT: Cromlish, Wanda A.  
; APPLICANT: Mancini, Joseph A.  
; APPLICANT: O'Neill, Gary  
; APPLICANT: Vickers, Philip J.  
; APPLICANT: Wong, Elizabeth  
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND  
; TITLE OF INVENTION: ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 Lincoln Avenue  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 in, 1.4kb  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7  
; SOFTWARE: Microsoft Word 5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/064,271  
; FILING DATE: 19930506  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Panzer, Curtis C.  
; REGISTRATION NUMBER: 33,752  
; REFERENCE/DOCKET NUMBER: 189061A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)594-3199  
; TELEFAX: (908)594-4720  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3387 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-064-271-11

Query Match 100.0%; Score 3387; DB 1; Length 3387;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 3361 TTAAGAGATTAAAAAAGAG 3387  
 Db 3361 TTAAGAGATTAAAAAAGAG 3387

## RESULT 2

US-09-023-655-1050

Sequence 1050, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilheimer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1050:

SEQUENCE CHARACTERISTICS:

LENGTH: 3387 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: G181253

US-09-023-655-1050

Query Match 99.8%; Score 3379; DB 4; Length 3387;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCCAGAAATCTCCACAGACGCTCTTCAAGCTTCACAGCAAGCCCTCAGACAGCA 60  
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Db 121 GTGGGCGGCTCTGGGCTCAGCCATACAGCAAAATCTTGCTTCCACCCATGTCAAA 180  
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DB 3361 TTAAAGATTTAAAAAAG 3387

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RESULT 3
US-08-627-254C-29
; Sequence 29, Application US/08627254C
; Patent No. 5859229
; GENERAL INFORMATION:
; APPLICANT: Kniss, Douglas A.
; TITLE OF INVENTION: Elcosanoid Formation
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griwold LLP
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,254C
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Golrick, Mary E
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 18525/00107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8200
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-627-254C-29

Query Match 99.7%; Score 3375.8; DB 2; Length 3387;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3380; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTCCAGAACTCTTAGAGAGGCGCTCTTCACTTCAAGCCAGACGCCCTTCAAGACAGA 60
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DB 121 GTGCGCGGCTCTGCGCGCTGAGCCATACAGCAATCTTGTCTTCCACCCATGTCAAA 180
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DB 181 GTGCGCGGCTCTGCGCGCTGAGCCATACAGCAATCTTGTCTTCCACCCATGTCAAA 180
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DB 241 ATTCTATGAGAACTGCTCAACACCGGAATTTTGAAGAATAATTAATTTCTGAA 300
QY 301 ACCCACTCCAAACAGAGCACTACATTAACCACTTCAAGGATTTTGAACGTGT 360
DB 301 ACCCACTCCAAACAGAGCACTACATTAACCACTTCAAGGATTTTGAACGTGT 360
QY 361 GAATTAACATTCCTCTCTTCAAAATGCAATTAATGATGATGTTGATGATTCAGATCA 420
DB 361 GAATTAACATTCCTCTCTTCAAAATGCAATTAATGATGATGTTGATGATTCAGATCA 420

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QY	421	TTTGATTGACAGTCCACCACCTAGATGCTGACTATGTGGCTACAAAAGCTGGAAAGCTT	480
Dp	421	TTTATATTGACAGTCCACCACCTTCAAAAGCTGACTATGTGGCTACAAAAGCTGGAAAGCTT	480
QY	481	CTTAACCTCTCCATTATTAAGTAGAGCCCTTCCTCTGTGCTGATGATGTTGCCAGATCC	540
Dp	481	CTTAACCTCTCTATTATTAAGTAGAGCCCTTCCTCTGTGCTGATGATGTTGCCAGATCC	540
QY	541	CTTGGGTCTCAAGGCTAAAAAGCAGCTTCTGATTCAAATGATGATTTGGAAAAATTGCT	600
Dp	541	CTTGGGTCTCAAAAGGTAATAAGAGCTTCTGATTCAAATGATGATTTGGAAAAATTGCT	600
QY	601	TCTAAGAAAGAGTTCAATCCCTGATGCCCAAGGCTCAAAATGATGATTTGCAATCTTTGC	660
Dp	601	TCTAAGAAAGAGTTCAATCCCTGATGCCCAAGGCTCAAAATGATGATTTGCAATCTTTGC	660
QY	661	CCAGACTCTACGCAACAGTTTTCACACAGATCATAGAGAGGGCCAGCTTTCACCA	720
Dp	661	CCAGACTCTACGCAATCAGTTTTCACACAGATCATAGAGAGGGCCAGCTTTCACCA	720
QY	721	CGGCTGGGCCATGGGGTGGACTTAATCATATTTACGCTGAAACTGTGCTGACAGCG	780
Dp	721	CGGCTGGGCCATGGGGTGGACTTAATCATATTTACGCTGAAACTGTGCTGACAGCG	780
QY	781	TAACTGGGCTTTCAAGATGGAAAAATGAAATATCAGATTAATTTGATGAGAGATGTA	840
Dp	781	TAACTGGGCTTTCAAGATGGAAAAATGAAATATGATTAATTTGATGAGAGATGTA	840
QY	841	TCCTCCACAGTCAAAAGTACTCAGGCAAGATGATCTACCTCCTCAAGTCCCTGAGCA	900
Dp	841	TCCTCCACAGTCAAAAGTACTCAGGCAAGATGATCTACCTCCTCAAGTCCCTGAGCA	900
QY	901	TCTACGTTTCTGTGGGGCAGAGGCTTTTGGTCTGTGCTGTGCTGATGATGATGC	960
Dp	901	TCTACGTTTCTGTGGGGCAGAGGCTTTTGGTCTGTGCTGTGCTGATGATGATGC	960
QY	961	CACATCTGGCTGGGGGAAACAACAAGATATGATGCTGTTAAACAGGAGCATCTCGA	1020
Dp	961	CACATCTGGCTGGGGGAAACAACAAGATATGATGCTGTTAAACAGGAGCATCTCGA	1020
QY	1021	ATGGGGTATGAGCAGTTGTTCCAGACAGCAGGCTAATATCTGATAGGAGACTATTTAA	1080
Dp	1021	ATGGGGTATGAGCAGTTGTTCCAGACAGCAGGCTAATATCTGATAGGAGACTATTTAA	1080
QY	1081	GATTGTGATTGAATTTATATGTGCACAACCTTAGTGGCTATCACTTCAAACTGAAATTGA	1140
Dp	1081	GATTGTGATTGAATTTATATGTGCACAACCTTAGTGGCTATCACTTCAAACTGAAATTGA	1140
QY	1141	CCGAGAACTACTTTTCAACAAACAATCCAGTACCAAAAATGTAATGTGCTGTAATTTAA	1200
Dp	1141	CCGAGAACTACTTTTCAACAAACAATCCAGTACCAAAAATGTAATGTGCTGTAATTTAA	1200
QY	1201	CACCTCTATCAGTCGCATCCCTCTTGCTGCTGACACCTTTCAAATTCATGACCAAAATA	1260
Dp	1201	CACCTCTATCAGTCGCATCCCTCTTGCTGCTGACACCTTTCAAATTCATGACCAAAATA	1260
QY	1261	CAACTATCAACAGTTTATCTACCAACATCTATATGTGTGGAACATGGAATTTACCAAGTT	1320
Dp	1261	CAACTATCAACAGTTTATCTACCAACATCTATATGTGTGGAACATGGAATTTACCAAGTT	1320
QY	1321	TGTTGAATCATTCACACAGGCAAAATTGCTGCGACAGGGTTGCTGTGTAGAGATGTTCCACC	1380
Dp	1321	TGTTGAATCATTCACACAGGCAAAATTGCTGCGACAGGGTTGCTGTGTAGAGATGTTCCACC	1380
QY	1381	CGCAGTACAGAAAGTATCACAGGCTTCATTGACCAGACAGGCGAGATGAATAACAGTC	1440
Dp	1381	CGCAGTACAGAAAGTATCACAGGCTTCATTGACAGCAGGCGAGATGAATAACAGTTC	1440
QY	1441	TTTTTAATGAGTACCGCAAAAGCCTTTATGCTGAAGCCTTATGAAATCATTTGAGAACTTAC	1500
Dp	1441	TTTTTAATGAGTACCGCAAAAGCCTTTATGCTGAAGCCTTATGAAATCATTTGAGAACTTAC	1500

QY	1501	AGGAGAAAAGAAATNGTGTGAGAGTTGGAAAGCACTGTATGCTGACATCGATGCGTGGGA	1560
Db	1501	AGGAGAAAAGAAATNGTGTGAGAGTTGGAAAGCACTGTATGCTGACATCGATGCGTGGGA	1560
QY	1561	GCTGTATCTCCCTTGTGTAGAAAAGCCCTGGCCAGATGCCATCTTTGGTGAAGCCAT	1620
Db	1561	GCTGTATCTCCCTTGTGTAGAAAAGCCCTGGCCAGATGCCATCTTTGGTGAAGCCAT	1620
QY	1621	GGTGAAGTTGGAGACACATCTCTCTGAAAGAGCTTATGGGTATGTTATATGTCTCC	1680
Db	1621	GGTGAAGTTGGAGACACATCTCTCTGAAAGAGCTTATGGGTATGTTATATGTCTCC	1680
QY	1681	TGCCCTACTGGAAGCCAAAGCACTTTTGGTGAGAAAGTGGGTTTCAATTCATCAACACTGC	1740
Db	1681	TGCCCTACTGGAAGCCAAAGCACTTTTGGTGAGAAAGTGGGTTTCAATTCATCAACACTGC	1740
QY	1741	CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGCTGTCCCTTACTTCATTCAGTGT	1800
Db	1741	CTCAATTCAGTCTCTCATCTGCAATTAACGTGAAGGGCTGTCCCTTACTTCATTCAGTGT	1800
QY	1801	TCCAGATCCAGAGCTCATTTAAACAGTCAACCATCAATGCAAGTCTCCCGCTCCGAGCT	1860
Db	1801	TCCAGATCCAGAGCTCATTTAAACAGTCAACCATCAATGCAAGTCTCCCGCTCCGAGCT	1860
QY	1861	AGATGATATCAATCCCAACAGTACTTAATAAAGAAACGGTCACTGACACTGTGAAGTCTAA	1920
Db	1861	AGATGATATCAATCCCAACAGTACTTAATAAAGAAACGGTCACTGACACTGTGAAGTCTAA	1920
QY	1921	TGATCATATTTATTTATTTATATGACCAAGTCTATTAATTTATTTATTAATTAATTTT	1980
Db	1921	TGATCATATTTATTTATTTATATGACCAAGTCTATTAATTTATTTATTAATTAATTTT	1980
QY	1981	ATATTTAAACTCCTTATGTATCTTAACATCTTCTGTAAACAGAAAGTCAGTACTCCGTGGCG	2040
Db	1981	ATATTTAAACTCCTTATGTATCTTAACATCTTCTGTAAACAGAAAGTCAGTACTCCGTGGCG	2040
QY	2041	GAGAAAGAGTCATACTTGTGAACACTTTATGTCACTACTTAAGATTTTGTCTGTTC	2100
Db	2041	GAGAAAGAGTCATACTTGTGAACACTTTATGTCACTACTTAAGATTTTGTCTGTTC	2100
QY	2101	TGTTAAGTTGGAAGACAGTTTATTTCTGTTTATTTAAACAGAGAGAAATGAGTTTGA	2160
Db	2101	TGTTAAGTTGGAAGACAGTTTATTTCTGTTTATTTAAACAGAGAGAAATGAGTTTGA	2160
QY	2161	CGTCTTTTACTTGAATTTCAACTTAATTTAAAGACGAAAGTAAAGATGTTTGAATAC	2220
Db	2161	CGTCTTTTACTTGAATTTCAACTTAATTTAAAGACGAAAGTAAAGATGTTTGAATAC	2220
QY	2221	TTAAACCTATCAACAAGTGCAAATGCGAAATGCTTAAACATCTGCGAATGTTTCCAAT	2280
Db	2221	TTAAACCTATCAACAAGTGCAAATGCGAAATGCTTAAACATCTGCGAATGTTTCCAAT	2280
QY	2281	GCATCTTCCATGATGCAATTAGAAAGTAACTATGTTTGAATTTTAAAGTACTTTTGGGTA	2340
Db	2281	GCATCTTCAATGATGCAATTAGAAAGTAACTATGTTTGAATTTTAAAGTACTTTTGGGTA	2340
QY	2341	TTTTTCTGTCTCAACAAACAAACAGGTATCACTGTCAATTTAAATGATATTTAAATTTGA	2400
Db	2341	TTTTTCTGTCTCAACAAACAAACAGGTATCACTGTCAATTTAAATGATATTTAAATTTGA	2400
QY	2401	CATTACCAAGTAACTTCACTGTCTAATTTTAAATCAAGCAATGAAACATATATTTGAATTT	2460
Db	2401	CATTACCAAGTAACTTCACTGTCTAATTTTAAATCAAGCAATGAAACATATATTTGAATTT	2460
QY	2461	TCATAATTCATAGGGTGAATCACTGTGAAGCTTGTGATTTCTTAAAGTTATTTAA	2520
Db	2461	TCATAATTCATAGGGTGAATCACTGTGAAGCTTGTGATTTCTTAAAGTTATTTAA	2520
QY	2521	CTTGTAACATATCCAAAGAAAGAGCTGTCTTGATTTAAATCTGTAAATCAAGATGAATTT	2580
Db	2521	CTTGTAACATATCCAAAGAAAGAGCTGTCTTGATTTAAATCTGTAAATCAAGATGAATTT	2580
QY	2581	TTACTACAAATGCTGTGTTAAATTTTATTAATGAGATGTTCTTTTCAACAAGATATA	2640

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Db      2581 TTACTCAATGCTGTGTAATAATTTTAAAGTATGTTCTTTTCCACCAAGAGTATA 2640
Qy      2641 AACCTTTTATGCTGCTGTTAAACCTCTTTTAAATCAAAATGCCAAATTATTAAG 2700
Db      2641 AACCTTTTATGCTGCTGTTAAACCTCTTTTAAATCAAAATGCCAAATTATTAAG 2700
Qy      2701 TGGTGGACCACTGCAAGTGTATCTCAAAATAAGATATCTGTTGAGATATTCAGAAAT 2760
Db      2701 TGGTGGACCACTGCAAGTGTATCTCAAAATAAGATATCTGTTGAGATATTCAGAAAT 2760
Qy      2761 CTGTTAATNGCTGGTAAATGTAATTAACCCCTATACCCCGCAAAAGGGCTTACCC 2820
Db      2761 CTGTTAATNGCTGGTAAATGTAATTAACCCCTATACCCCGCAAAAGGGCTTACCC 2820
Qy      2821 TTGAACATTAAGCAATTAACCAAAAGAGAAAGCCCAATTTATGTTCCAAATTTAGGT 2880
Db      2821 TTGAACATTAAGCAATTAACCAAAAGAGAAAGCCCAATTTATTTAGGT 2880
Qy      2881 TTAACTTTTGAAGCAAACTTTTGTGACCTTTGACAGTGCAGACTGTAAGT 2940
Db      2881 TTAACTTTTGAAGCAAACTTTTGTGACCTTTGACAGTGCAGACTGTAAGT 2940
Qy      2941 TTTCATAGAGGTAAATGAAGCAAGCTGCTGATTAAGATATGTTTCTAGAT 3000
Db      2941 TTTCATAGAGGTAAATGAAGCAAGCTGCTGATTAAGATATGTTTCTAGAT 3000
Qy      3001 TTTCCTGTGACAGTTAATTTAGCAAGTGCATATCACTGCAAAAGTGAATGACCTC 3060
Db      3001 TTTCCTGTGACAGTTAATTTAGCAAGTGCATATCACTGCAAAAGTGAATGACCTC 3060
Qy      3061 ATAAATACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTTCTAGCTTG 3120
Db      3061 ATAAATACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTTCTAGCTTG 3120
Qy      3121 AAGCCATTCAGAGTGTGATGATCAAGCTGCTGACCTGCTGCTGCTGCTGCTGCT 3180
Db      3121 AAGCCATTCAGAGTGTGATGATCAAGCTGCTGACCTGCTGCTGCTGCTGCTGCT 3180
Qy      3181 TTTCCTGTGACAGTTAATTTAGCAAGTGCATATCACTGCAAAAGTGAATGACCTC 3240
Db      3181 TTTCCTGTGACAGTTAATTTAGCAAGTGCATATCACTGCAAAAGTGAATGACCTC 3240
Qy      3241 TTTCCTGTGACAGTTAATTTAGCAAGTGCATATCACTGCAAAAGTGAATGACCTC 3300
Db      3241 TTTCCTGTGACAGTTAATTTAGCAAGTGCATATCACTGCAAAAGTGAATGACCTC 3300
Qy      3301 TACCTGAAGCTTTGCAAGTGTGCAAGTGAACCTGCAAGCTGCTGCTGCTGCTGCT 3360
Db      3301 TACCTGAAGCTTTGCAAGTGTGCAAGTGAACCTGCAAGCTGCTGCTGCTGCTGCT 3360
Qy      3361 TTAAAGAGATTAATAAAAAAAAAAAG 3387
Db      3361 TTAAAGAGATTAATAAAAAAAAAAAG 3387

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# RESULT 4

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US-08-930-589A-19
; Sequence 19, Application US/08930589A
; Patent No. 6107087
; GENERAL INFORMATION:
; APPLICANT: MERCK FROST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; TITLE OF INVENTION: CYCLOOXYGENASE-2
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA

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; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,589A
; FILING DATE: 28-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A.
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19029PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-930-589A-19

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Query Match          99.6%; Score 3374.2; DB 3; Length 3387;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3379; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy      1 GTTCAGAGAACTCTTCAAGAGCGCTCTTCACTGCTCAACGCCAGCGCTTGAAGACA 60
Db      1 GTTCAGAGAACTCTTCAAGAGCGCTCTTCACTGCTCAACGCCAGCGCTTGAAGACA 60
Qy      61 AAGCCTAACCCCGCGCGCGCGCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCTGCT 120
Db      61 AAGCCTAACCCCGCGCGCGCGCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCTGCT 120
Qy      121 GTGCGCGGTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCT 180
Db      121 GTGCGCGGTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCT 180
Qy      181 CCGAGGTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db      181 CCGAGGTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy      241 ATTCTATGAGAAATGCTGCTCAACCGGAATTTTGAACAATTAATTAATTTCTGAA 300
Db      241 ATTCTATGAGAAATGCTGCTCAACCGGAATTTTGAACAATTAATTAATTTCTGAA 300
Qy      301 ACCCACTCCAAACAGAGTCACTAATCACTTCAACCGGATTTTGAACGTTGT 360
Db      301 ACCCACTCCAAACAGAGTCACTAATCACTTCAACCGGATTTTGAACGTTGT 360
Qy      361 GAATAAATTCCTCTCTTCTGCAAAATGCAATTAATGATTAATGATTAATGATTAAT 420
Db      361 GAATAAATTCCTCTCTTCTGCAAAATGCAATTAATGATTAATGATTAATGATTAAT 420
Qy      421 TTGATGAGACGTGCAACCACTTAATCAATGCTGATGCTGCAAAAGCTGGAAAGCTT 480
Db      421 TTGATGAGACGTGCAACCACTTAATCAATGCTGATGCTGCAAAAGCTGGAAAGCTT 480
Qy      481 CTCTAACTCTCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Db      481 CTCTAACTCTCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Qy      541 CTGAGGTGTCAAAAGTAAAGCAAGCTTCTGATTAATTAATTAATTAATTAATTAAT 600
Db      541 CTGAGGTGTCAAAAGTAAAGCAAGCTTCTGATTAATTAATTAATTAATTAATTAAT 600

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QY 601 TCTAAGAGAAAGTTCATCCCTGATCCCGAGGCTCAACATGATGTTTCATCTCTTGC 660  
DB 601 TCTAAGAGAAAGTTCATCCCTGATCCCGAGGCTCAACATGATGTTTCATCTCTTGC 660  
QY 661 CCAGCATCTTGAGCAGCAGGATTTTCAAGACATCATTAAGCAGGCGACCTTTCACCA 720  
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DB 721 CGGAGCTGGGCGCAGGAGTGAAGTAAATCAATTTACGTTGAAGTCTGGCTGACAGCG 780  
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DB 781 TAAAGTCGCGCTTTCAAGAGATGAAAAATGAATATCAGATTAATGATGAGACATGTA 840  
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DB 901 TCTAAGGTTTGTGCTGGGCGAGGAGTCTTGTGCTGGGCTGATGATGATGATG 960  
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DB 961 CACAATCTGGCTCGGAGAACACAGAGATGATGCTGATGCTTAAACAGAGATCTCTGA 1020  
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DB 1021 ATGAGGATGATGAGCAGTGTTCAGACACAGAGCTTAATCTGATAGAGACATTA 1080  
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DB 1081 GATTGATGATGAGATTAATGATGACACTGATGCTGATCACTTGAACCTGAAATTTGA 1140  
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DB 1201 CACCTCTCATCATGCGATCCCTTCTGCTGACACCTTTCAATTCATGACAGAAAT 1260  
QY 1261 CAACCTCATCACTGCGATCCCTTCTGCTGACACCTTTCAATTCATGACAGAAAT 1320  
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DB 1321 TGTGATCATTCACAGGCAATTCCTGGAGGGTGTGCTGGTGGTGAAGATTTCCACC 1380  
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DB 1381 CGCAGTACAGAAAGTATCACAGGCTTCATGACAGAGAGGAGAGATGAATACAGATC 1440  
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DB 1441 TTTTAAATGATGACCGCAAAAGCTTTATGCTGAAGCCCTATGAATCATTTGAAGAACTTAC 1500  
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DB 1501 AAGAGAAAAGAAATGTGACAGAGTGAAGCACTATGCTGACATGATGCTGTGA 1560  
QY 1561 GCTGTATCTGCTCTTCTGCTGAGAAAAAGCTGGCAGAGTGCATCTTTGGTGAACCAT 1620  
DB 1561 GCTGTATCTGCTCTTCTGCTGAGAAAAAGCTGGCAGAGTGCATCTTTGGTGAACCAT 1620  
QY 1621 GGTAGAAAGTTGAGACCAATCTCTCTTGAAGGACTTAAGGATTAATGATTAATGCTCC 1680  
DB 1621 GGTAGAAAGTTGAGACCAATCTCTCTTGAAGGACTTAAGGATTAATGATTAATGCTCC 1680

QY 1681 TGCTTACTGGAAGCCAGACACTTTTGTGAGAGAGTGGGTTTCAATCATCAACACTGC 1740  
DB 1681 TGCTTACTGGAAGCCAGACACTTTTGTGAGAGAGTGGGTTTCAATCATCAACACTGC 1740  
QY 1741 CTCATTCAGTCTCTCATCTGCAATTAACGTGAAGGCTGTCCCTTACTTCAATTCAGTGT 1800  
DB 1741 CTCATTCAGTCTCTCATCTGCAATTAACGTGAAGGCTGTCCCTTACTTCAATTCAGTGT 1800  
QY 1801 TCCAGATCCAGAGTCTATTAACCAATCATGCAAGTCTTCCCGCTCGGAGCT 1860  
DB 1801 TCCAGATCCAGAGTCTATTAACCAATCATGCAAGTCTTCCCGCTCGGAGCT 1860  
QY 1861 AGATGATCAATCCACAGTACTACTTAAAGAACGCTGCACTGAAGTGAAGCTTAA 1920  
DB 1861 AGATGATCAATCCACAGTACTACTTAAAGAACGCTGCACTGAAGTGAAGCTTAA 1920  
QY 1921 TGATCAATTAATTTATTAATATGAACCATGTCTATTAATTAATTAATTAATTT 1980  
DB 1921 TGATCAATTAATTTATTAATATGAACCATGTCTATTAATTAATTAATTAATTT 1980  
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DB 1981 ATATTAACTCCTTATGTTACTTAAATCATCTCTGTAACAGAGTCACTCCTGTGCG 2040  
QY 2041 GAGAAAGAGTCAATCTTGTAAGACCTTTATGTCATCTTAAAGATTTTGTCTGTC 2100  
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QY 2461 TCTAATTCATAGGGTGAATCACTGTAAAGCTTTGATTTCTTAAAGTATTA 2520  
DB 2461 TCTAATTCATAGGGTGAATCACTGTAAAGCTTTGATTTCTTAAAGTATTA 2520  
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DB 2521 CTTGATCATATCAAAAGAAAGCTGCTGATTTAAATCGTAAATCGATGAAT 2580  
QY 2581 TTAATCAATTCCTGTTAAATTTATTAAGATGTTCTTTTCAACAAAGATATA 2640  
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QY 2641 AACCTTTTAAAGTGTGCTTAAACTTCTTTTAAATCAAAATGCAATTTATTAAG 2700  
DB 2641 AACCTTTTAAAGTGTGCTTAAACTTCTTTTAAATCAAAATGCAATTTATTAAG 2700  
QY 2701 TGTGAGGCACTGCAAGTGTATCTCAAAATTAAGATATCTGTTGAAGATTTCCGAAT 2760  
DB 2701 TGTGAGGCACTGCAAGTGTATCTCAAAATTAAGATATCTGTTGAAGATTTCCGAAT 2760  
QY 2761 CTGTTATATGCTGTGAATGTAATTAACCCCATTAACCCCGCAAAAGGGGTCTTACC 2820



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Db      2761  CTGTTATATGCTGTATACATGTAATAAAACCCCATTAACCCCGCAAAAGGGCTCTACCC 2820
Qy      2821  TTGAACATAAGCAATATACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAAGGT 2880
Db      2821  TTGAACATAAGCAATATACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAAGGT 2880
Qy      2881  TTAACCTTTTGAAGCAAACTTTTATGACCTTGTGACCTGACAGCTGACTCAGAT 2940
Db      2881  TTAACCTTTTGAAGCAAACTTTTATGACCTTGTGACCTGACAGCTGACTCAGAT 2940
Qy      2941  TTGCTATGAGGTATATGAAGTACCAAGCTGTGCTTGAATTAAGATATGTTTTCAGAT 3000
Db      2941  TTGCTATGAGGTATATGAAGTACCAAGCTGTGCTTGAATTAAGATATGTTTTCAGAT 3000
Qy      3001  TTTCTGTGTAGAGTTAATTTATAGAGTCAATATATGCAATGCAAAAGTAGCAATACCTC 3060
Db      3001  TTTCTGTGTAGAGTTAATTTATAGAGTCAATATATGCAATGCAAAAGTAGCAATACCTC 3060
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Db      3061  ATAAATAACCTCTTCAAAATGCTTAATTCATTTTCAACATTTATTTATCTCAGTCTTG 3120
Qy      3121  AAGCAATTCAGTATGATGCTATGGAATCAAGCTGTGCTTGAATGCTGATGCTTCTTCT 3180
Db      3121  AAGCAATTCAGTATGATGCTATGGAATCAAGCTGTGCTTGAATGCTGATGCTTCTTCT 3180
Qy      3181  TTTCTCTTTTACGATTTTGTGTAAGAGACAGATCTTCTGAAACATCTGTTTCTCTA 3240
Db      3181  TTTCTCTTTTACGATTTTGTGTAAGAGACAGATCTTCTGAAACATCTGTTTCTCTA 3240
Qy      3241  TTTTGTATTTAGTATTTAAGATCAGAGTTCATTTCTTTGACCTGCTCAATATTTTCT 3300
Db      3241  TTTTGTATTTAGTATTTAAGATCAGAGTTCATTTCTTTGACCTGCTCAATATTTTCT 3300
Qy      3301  TACCTGAATTTTGAAGTTTTCAGGTAACTGCTCAGAGTCTGATTTAGTCTCTC 3360
Db      3301  TACCTGAATTTTGAAGTTTTCAGGTAACTGCTCAGAGTCTGATTTAGTCTCTC 3360
Qy      3361  TTAAGAGATTAATAAAAAAAAAAAAAAG 3387
Db      3361  TTAAGAGATTAATAAAAAAAAAAAAAAG 3387

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RESULT 5
US-09-599-781-19
; Sequence 19, Application US/09599781
; Patent No. 6362327
GENERAL INFORMATION:
APPLICANT: MERCK FROST CANADA & CO.
O'NEILL, GARY P.
MANCINI, JOSEPH A.
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
CYCLOOXYGENASE-2
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PASESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,781
FILING DATE: 21-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,033

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; FILING DATE: 27-Sep-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19029PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELE: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-599-781-19

Query Match      99.6% Score 3374.2; DB 4; Length 3387;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3379; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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181  CCGAGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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241  ATTCTATGAGAAATAATGCTCTCAACACCGGAAATTTTGAAGAATAATTTTCTGAA 300
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## RESULT 6

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US-08-487-753-3
; Sequence 3, Application US/08487753
; Patent No. 5807733
; GENERAL INFORMATION:
; APPLICANT: Young, Donald A.
; APPLICANT: O'Banion, Michael K.
; APPLICANT: Winn, Virginia D.
; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,753
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3996-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ. ID NO.: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1834 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-487-753-3
Query Match 53.2%; Score 1803.2; DB 1; Length 1834;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1814; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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Db	601	CAGATCATTAAGGAGGGCCAGCTTTACCAACGGGCTGGGCCATGGGATGGACTTAATC	660
QY	750	AATATTTAGGGTAAACTCTGGCTAGACAGCTTAACTGGGCTTTTCAAGATTCGAAAA	809
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RESULT 8			
US-08-480-065-3			
Sequence 3, Application US/08480065			
Patent No. 5837479			
GENERAL INFORMATION:			
APPLICANT: Young, Donald A.			
APPLICANT: O'Banion, Michael K.			
TITLE OF INVENTION: SCREENING ASSAYS FOR INHIBITORS OF			
TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2			
NUMBER OF SEQUENCES: 18			
CORRESPONDENCE ADDRESS:			
ADDRESSER: Pennie & Edmonds			
STREET: 1155 Avenue of the Americas			
CITY: New York			
STATE: New York			
COUNTRY: U.S.A.			
ZIP: 10036-2711			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patencin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/480,065			
FILING DATE: 07-JUN-1995			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: Coruzzi, Laura A.			
REGISTRATION NUMBER: 30,742			
REFERENCE/DOCKET NUMBER: 3996-012			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (212) 790-9090			
TELEFAX: (212) 869-9741/8864			
TELEX: 66141 PENNIE			
INFORMATION FOR SEQ ID NO: 3:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1834 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: unknown			
MOLECULE TYPE: DNA (genomic)			
US-08-480-065-3			
Query Match			
Best Local Similarity			
Matches 1814, Conservative 0, Mismatches 18, Indels 0, Gaps 0,			
QY	90	CCGCTGGAGGCTCCGCCCGCCCTGCTGTGCGCCGCTCCGGCGCTTACGCCATACAG	149
Db	1	CCGCTGGAGGCTCCGCCCGCCCTGCTGTGCGCGGCTCCGGCGCTTACGCCATACAG	60
QY	150	CAATCTCTCTCTCCACCCATGTCAAAACGAGGTGATATGATGATGGAGTTTG	209
Db	61	CAATCTCTCTCTCTCCACCCATGTCAAAACGAGGTGATATGATGATGGAGTTTG	120
QY	210	ACCAAGTAAAGTGCGATTTGATCCCGGACAGAGATTTCTATGGAGAAAATGCTCAACCGG	269
Db	121	ACCAAGTAAAGTGCGATTTGATCCCGGACAGAGATTTCTATGGAGAAAATGCTCAACCGG	180

QY 270 AATTTTGAAGATTAATTTATTTCTGAACCCACTTCCAAACACAGTGCATCTATAC 323  
 Db 181 AATTTTGAAGATTAATTTATTTCTGAACCCACTTCCAAACACAGTGCATCTATAC 240  
 QY 330 TTACCACTTCAAGGATTTTGAAGCTTGTGATATACATTCCTCTCCATGCAATGCA 389  
 Db 241 TTACCACTTCAAGGATTTTGAAGCTTGTGATATACATTCCTCTCCATGCAATGCA 300  
 QY 390 TTATGATTAATGTGATGATCAGATCAATTTGATGACAGTCCACCACTTACAAATG 449  
 Db 301 TTATGATTAATGTGATGATCAGATCAATTTGATGACAGTCCACCACTTACAAATG 360  
 QY 450 CTGATATAGCTGACAAAGCTGGGAAAGCTTCTAACCTCTCCATTAATTAAGAGCC 509  
 Db 361 CTGATATAGCTGACAAAGCTGGGAAAGCTTCTAACCTCTCCATTAATTAAGAGCC 420  
 QY 510 TTCCCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 569  
 Db 421 TTCCCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 QY 570 CTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 629  
 Db 481 CTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
 QY 630 AGGCTCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 689  
 Db 541 AGGCTCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 QY 690 CAGATCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 749  
 Db 601 CAGATCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 QY 750 ATATTGAAGTGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATG 809  
 Db 661 ATATTGAAGTGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATG 720  
 QY 810 TGAATATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 869  
 Db 721 TGAATATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 QY 870 AGATGATCACTCCCTCTCAAGTCCCTGAGATCTACGCTTCTGCTGCTGCTGCTG 929  
 Db 781 AGATGATCACTCCCTCTCAAGTCCCTGAGATCTACGCTTCTGCTGCTGCTGCTG 840  
 QY 930 TTGCTGCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 989  
 Db 841 TTGCTGCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 900  
 QY 990 TATGATGATGCTTAAACAGAGGATCCGATGAGGAGTGAAGAGTGTTCAGAGCA 1049  
 Db 901 TATGATGATGCTTAAACAGAGGATCCGATGAGGAGTGAAGAGTGTTCAGAGCA 960  
 QY 1050 GCAGGCTAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1109  
 Db 961 GCAGGCTAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
 QY 1110 TGAAGTGGCTATCACTTCAAACTGAAATTTGACCCAGACTACTTTTCAACAACTTC 1169  
 Db 1021 TGAAGTGGCTATCACTTCAAACTGAAATTTGACCCAGACTACTTTTCAACAACTTC 1080  
 QY 1170 AGTACCAAAATGATGATGCTGCTGATGATGATGATGATGATGATGATGATGATG 1229  
 Db 1081 AGTACCAAAATGATGATGCTGCTGATGATGATGATGATGATGATGATGATGATG 1140  
 QY 1230 CTGACACCTTCAAAATCTGACAGAAATATACATATCAAGATTTATCTACAACT 1289  
 Db 1141 CTGACACCTTCAAAATCTGACAGAAATATACATATCAAGATTTATCTACAACT 1200  
 QY 1290 CTATATGCTGGAACATGGAATTTACCAAGTTGTTGATCATTTACACAGGCAATTTGCTG 1349  
 Db 1201 CTATATGCTGGAACATGGAATTTACCAAGTTGTTGATCATTTACACAGGCAATTTGCTG 1260

QY 1350 GCAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1409  
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 Db 1321 TTGACAGAGAGGAGAGATGAAATACAGATCTTTTAAATGATGATGATGATGATG 1380  
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 Db 1381 TGAAGCTTATGATCATTTTGAAGACTTACAGAGAAAGAAATGCTGAGATG 1440  
 QY 1530 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1589  
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 QY 1650 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1709  
 Db 1561 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
 QY 1710 GAGAAGTGGTCTTCAATCATCAACACTGCTCAATCAGTCTCTCATCTGCAATTA 1769  
 Db 1621 GAGAAGTGGTCTTCAATCATCAACACTGCTCAATCAGTCTCTCATCTGCAATTA 1680  
 QY 1770 TGAAGGCTGCTGCTTCAATCATCAACACTGCTCAATCAGTCTCTCATCTGCA 1829  
 Db 1681 TGAAGGCTGCTGCTTCAATCATCAACACTGCTCAATCAGTCTCTCATCTGCA 1740  
 QY 1830 CCATCAATGCAAGTCTTCCGCTCCGATGATGATGATGATGATGATGATGATGATG 1889  
 Db 1741 CCATCAATGCAAGTCTTCCGCTCCGATGATGATGATGATGATGATGATGATG 1800  
 QY 1890 AAGAACGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1921  
 Db 1801 AAGAACGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1832

RESULT 9  
 US-08-480-065-14  
 ; Sequence 14, Application US/08480065  
 ; Patent No. 5837479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Donald A.  
 ; APPLICANT: O'Banion, Michael K.  
 ; APPLICANT: Winn, Virginia D.  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR INHIBITORS OF  
 ; MAMMALIAN PROTAGLANDIN H SYNTHASE-2  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/480,065  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cornuzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 3996-012  
 ; TELECOMMUNICATION INFORMATION:





APPLICANT: Young, Donald A.  
APPLICANT: O'Banion, Michael K.  
TITLE OF INVENTION: METHODS FOR INHIBITING PROTAGLANDIN  
TITLE OF INVENTION: METHODS FOR INHIBITING PROTAGLANDIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,744  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Cornuzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3996-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 780-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1834 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-487-744-3

Query Match 53.2%; Score 1803.2; DB 3; Length 1834;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 1814; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 90 CCGCTGCGATGCTGCGCCGCGCCCTGCTGTCGCGCGTCTGCGGCTCAGCCATACAG 149  
DB 1 CCGCTGCGATGCTGCGCCGCGCCCTGCTGTCGCGCGTCTGCGGCTCAGCCATACAG 60  
QY 150 CAAATCTTCTGCTGCTCCACCCATGTCMAAACCGAGGTGATGATGAGTGTGGATTGG 209  
DB 61 CAAATCTTCTGCTGCTCCACCCATGTCMAAACCGAGGTGATGATGAGTGTGGATTGG 120  
QY 210 ACCAGATATAGTGCATGTAACCCGAGAGATTTATGAGAAACCTGCTCAACACCGG 269  
DB 121 ACCAGATATAGTGCATGTAACCCGAGAGATTTATGAGAAACCTGCTCAACACCGG 180  
QY 270 AATTTTGAACAAGATTAATTTCTGAAACCACTCCAAACAGAGTGCATACATAC 329  
DB 181 AATTTTGAACAAGATTAATTTCTGAAACCACTCCAAACAGAGTGCATACATAC 240  
QY 330 TTAACCACTTCAAGGATTTTGAAGCTTGAATTAACATTCCTTCTTCCAAATGCAA 389  
DB 241 TTAACCACTTCAAGGATTTTGAAGCTTGAATTAACATTCCTTCTTCCAAATGCAA 300  
QY 390 TATAGATATAGTGCATGTAACCATTCATTTGATGACATGCAACCACTTCAATG 449  
DB 301 TATAGATATAGTGCATGTAACCATTCATTTGATGACATGCAACCACTTCAATG 360  
QY 450 CTGACATATGAGCTCAAAAGCTGGGAAGCCTTCTTAACCTTCTTAATTAATACAGGCC 509  
DB 361 CTGACATATGAGCTCAAAAGCTGGGAAGCCTTCTTAACCTTCTTAATTAATACAGGCC 420  
QY 510 TTCTCTCTGTGCTGATGATGCTGCGGATCTCCTTGGGTGTCAAAAGTAAAGCAGCTTC 569

DB 421 TTCTCTCTGTGCTGATGATGCTGCGGATCTCCTTGGGTGTCAAAAGTAAAGCAGCTTC 480  
QY 570 CTGATTCATATGAGATTTGGAAAAATTTGCTTAAAGAAAGTTCATCTCTGATCCCC 629  
DB 481 CTGATTCATATGAGATTTGGAAAAATTTGCTTAAAGAAAGTTCATCTCTGATCCCC 540  
QY 630 AGGGCTCAACATGATGTTTGCATCTTCTTCCAGACCTCAGGACCAAGTTTTCAGA 689  
DB 541 AGGGCTCAACATGATGTTTGCATCTTCTTCCAGACCTCAGGACCAAGTTTTCAGA 600  
QY 690 CAGATCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 749  
DB 601 CAGATCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
QY 750 ATATTTAAGGTGAAATCTGCTGCTAGACAGGCTTAACTGGGCTTTCAGAGTGAAGAA 809  
DB 661 ATATTTAAGGTGAAATCTGCTGCTAGACAGGCTTAACTGGGCTTTCAGAGTGAAGAA 720  
QY 810 TGAATATCAGATTAATTTGATGAGAGATGATATCTCCACAGTCAAGATTAATCAAGGAG 869  
DB 721 TGAATATCAGATTAATTTGATGAGAGATGATATCTCCACAGTCAAGATTAATCAAGGAG 780  
QY 870 AGATGATTAACCTCTCTCAAGTCCCTGAGCATCTACGTTTGTGTGGGAGAGAGTCT 929  
DB 781 AGATGATTAACCTCTCTCAAGTCCCTGAGCATCTACGTTTGTGTGGGAGAGAGTCT 840  
QY 930 TTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 989  
DB 841 TTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 990 TATGATGATGCTTAAACAGAGCATCTGAATGGGGTATGAGCAGTTTTCAGACAA 1049  
DB 901 TATGATGATGCTTAAACAGAGCATCTGAATGGGGTATGAGCAGTTTTCAGACAA 960  
QY 1050 GCAGGCTAATTAATGATGAGAGAGCATTTAATGATGATGATGATGATGATGATGAT 1109  
DB 961 GCAGGCTAATTAATGATGAGAGAGCATTTAATGATGATGATGATGATGATGATGAT 1020  
QY 1110 TGATGCTGATCATCTTCAAACTGAATTTGACCCCAACATCTTTCACAAACATTTCC 1169  
DB 1021 TGATGCTGATCATCTTCAAACTGAATTTGACCCCAACATCTTTCACAAACATTTCC 1080  
QY 1170 AGTACCAAAATGATATGCTGCTGATTTTAAACCTCTATACATGCGATCCCTCTCG 1229  
DB 1081 AGTACCAAAATGATATGCTGCTGATTTTAAACCTCTATACATGCGATCCCTCTCG 1140  
QY 1230 CTGACACCTTTCAAACTTATGACAGAAATTAACAATTAACAATTTATCTACAAACT 1289  
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QY 1290 CTATATTTGCTGGAACATGGAATTAACCACTTTGTTGAATCATTCACAGGCAAAATGCTG 1349  
DB 1201 CTATATTTGCTGGAACATGGAATTAACCACTTTGTTGAATCATTCACAGGCAAAATGCTG 1260  
QY 1350 GCAGGCTTCTGCTGCTGGAATTTTCAACCCGAGTACAGAAAGTATACAGGCTTCCA 1409  
DB 1261 GCAGGCTTCTGCTGCTGGAATTTTCAACCCGAGTACAGAAAGTATACAGGCTTCCA 1320  
QY 1410 TTGACCAAGAGCAGGAGATGAAATTAACAGTCTTTTAAAGTACCGCAAAAGCTTTATGC 1469  
DB 1321 TTGACCAAGAGCAGGAGATGAAATTAACAGTCTTTTAAAGTACCGCAAAAGCTTTATGC 1380  
QY 1470 TGAAGCCCTATGATATTTGAAGAACTTAAGAGAAAGAAAGTCTGACAGATTTG 1529  
DB 1381 TGAAGCCCTATGATATTTGAAGAACTTAAGAGAAAGAAAGTCTGACAGATTTG 1440  
QY 1530 AAGCACTATAGTGCATGATGCTGTGAGCTGATCTGCTTCTGTTAGAAAGC 1589  
DB 1441 AAGCACTATAGTGCATGATGCTGTGAGCTGATCTGCTTCTGTTAGAAAGC 1500  
QY 1590 CTGCGCAATGCACTCTTTGTTGAAACATAGTGTGAAGTGTGAAGACCATTTCTCTTGA 1649  
DB 1501 CTGCGCAATGCACTCTTTCTTCAAAACATCTTCAAACTTGAAGACCATTTCTCTTGA 1560





QY	1230	TTGACACGCTTTGCAATTCATGACGACGAAATACACTTCACAGCTTATCTACAACACT	1289
Db	1141	CTGACACGCTTTGCAATTCATGACGACGAAATACACTTCACAGCTTATCTACAACACT	1200
QY	1290	CTATATATGCTGGAACAATGGAATTAACCAAGTTTGTGTAATCATTCACCAAGCAATGCTG	1349
Db	1201	CTATATATGCTGGAACAATGGAATTAACCAAGTTTGTGTAATCATTCACCAAGCAATGCTG	1260
QY	1350	GCAGGGTTGCTGTGTGTAGAAATGTTCCACCCGAGTACGAAAGTATCCAGAGCTTCCA	1409
Db	1261	GCAGGGTTGCTGTGTGTAGAAATGTTCCACCCGAGTACGAAAGTATCCAGAGCTTCCA	1320
QY	1410	TTGACCAAGACAGGACAGATGAAATACCAAGTCTTTTAATGAGTACCGCAAAAGCTTTATGC	1469
Db	1321	TTGACCAAGACAGGACAGATGAAATACCAAGTCTTTTAATGAGTATCCGCAAAAGCTTTATGC	1380
QY	1470	TGAAGCCCTTATGATTCATTTTGAAGAACCTTACAGAGAGAAAGAAATGTCTGCAAGTTGG	1529
Db	1381	TGAAGCCCTTATGATTCATTTTGAAGAACCTTACAGAGAGAAAGAAATGTCTGCAAGTTGG	1440
QY	1530	AAGCACTCTATGTGTGACATCGATGCTGTGAGCTGTATCTCGCCCTTCTGTAGAGAAAAGC	1589
Db	1441	AAGCACTCTATGTGTGACATCGATGCTGTGAGCTGTATCTCGCCCTTCTGTAGAGAAAAGC	1500
QY	1590	CTGGGCCAGATGCCATCTTTTGTGTAAACCAATGTGTAGAGTTGGAGACACATTCCTCTTGA	1649
Db	1501	CTGGGCCAGATGCCATCTTTTGTGTAAACCAATGTGTAGAGTTGGAGACACATTCCTCTTGA	1566
QY	1650	AAGCACTTATGTGTGATTTGTTATATGTTCTCTGCTACTGTGAAGCCAAAGCACTTTTGGTG	1709
Db	1561	AAGCACTTATGTGTGATTTGTTATATGTTCTCTGCTACTGTGAAGCCAAAGCACTTTTGGTG	1620
QY	1710	GAGAAGTGGGTTTTCAAAATCAATCAACACTGCTCAATTCAGTCTCTCATCTGCAATTAACG	1765
Db	1621	GAGAAGTGGGTTTTCAAAATCAATCAACACTGCTCAATTCAGTCTCTCATCTGCAATTAACG	1680
QY	1770	TGAAGGGGTGTCCTCTTACTTCATTCAGTGTCCAGATCCAGAGCTCATTTAAACAGTCA	1823
Db	1681	TGAAGGGGTGTCCTCTTACTTCATTCAGTGTCCAGATCCAGAGCTCATTTAAACAGTCA	1740
QY	1830	CCATCAATGCAAGTTCTTCCCGCTCCGACCTAGATGATATCAATCCACAGTACTTACTTA	1887
Db	1741	CCATCAATGCAAGTTCTTCCCGCTCCGACCTAGATGATATCAATCCACAGTACTTACTTA	1800
QY	1890	AAGAAAGCTGCAGCTGACATGTGTAGAGTCTAAT	1921
Db	1801	AAGAAAGCTGCAGCTGACATGTGTAGAGTCTAAT	1832

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FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Woessner, Warren D.  
 REGISTRATION NUMBER: 30,440  
 REFERENCE/DOCKET NUMBER: 8840.20-US-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEFAX: 612-332-9081  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1834 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Human PGHS-2

Query Match	53.2%	Score 1803.2	DB 5	Length 1834
Best Local Similarity	99.0%	Pred. No. 0	Mismatches 18	Indels 0
Matches 1814	Conservative 0			Gaps 0
QY	90	CCGCTGCGATGCTGCGCCGCGCCCTGCTGCTGTCGCGGTCTTGAGCTGACGCTACAG	149	
Db	1	CCGCTGCGATGCTGCGCCGCGCCCTGCTGCTGTCGCGGTCTTGAGCTGACGCTACAG	60	
QY	150	CAATTCCTGCTGTTCCCAACCATGTCAAAACGAGGTGTATGTATGATGCTGGATTGG	209	
Db	61	CAATTCCTGCTGTTCCCAACCATGTCAAAACGAGGTGTATGTATGATGCTGGATTGG	120	
QY	210	ACCAATATAGTGGATTTGACCCGAGACGAGATTCTATNGAGAAAACMGCTCAACCGG	269	
Db	121	ACCAATATAGTGGATTTGACCCGAGACGAGATTCTATNGAGAAAACMGCTCAACCGG	180	
QY	270	AATTTTGAACAAGATTAATAATTTCTGAAACCCACTCCAAACAGCTGCACTACATAC	329	
Db	181	AATTTTGAACAAGATTAATAATTTCTGAAACCCACTCCAAACAGCTGCACTACATAC	240	
QY	330	TTACCCACTCAAGGGATTTTGGAAACGTGTGAATATACATTCCTCTTGAAATGCAA	389	
Db	241	TTACCCACTCAAGGGATTTTGGAAACGTGTGAATATACATTCCTCTTGAAATGCAA	300	
QY	390	TTATGATTAATGTGTGAATCATGCAGATCAATTTGATGACGTCCACCACTTACAAAG	449	
Db	301	TTATGATTAATGTGTGAATCATGCAGATCAATTTGATGACGTCCACCACTTACAAAG	360	
QY	450	CTGACTATGCTCAAAAAGCTTGGAAAGCTTCTTAACCTCTCCATTAATACTAAGGCC	509	
Db	361	CTGACTATGCTCAAAAAGCTTGGAAAGCTTCTTAACCTCTCCATTAATACTAAGGCC	420	
QY	510	TTCTCTCTGTCGCTGATGATTTGGCCGACCTCCCTTGAGGTGTCAAAGGTAAAGACGCTTC	569	
Db	421	TTCTCTCTGTCGCTGATGATTTGGCCGACCTCCCTTGAGGTGTCAAAGGTAAAGACGCTTC	480	
QY	570	CTGATTCAAATAGATTTGGAAAAATTGCTTCTTAAGAAAGATTCATCCCTGATCCCC	629	
Db	481	CTGATTCAAATAGATTTGGAAAAATTGCTTCTTAAGAAAGATTCATCCCTGATCCCC	540	
QY	630	AGGGCTCAAAACATGATGTTTGCAATCTTTGGCCAGCACTTCACGCAACAGTTTTTCAAGA	689	
Db	541	AGGGCTCAAAACATGATGTTTGCAATCTTTGGCCAGCACTTCACGCAACAGTTTTTCAAGA	600	
QY	690	CAGATCATTAAGGAGGGCCAGCTTTACCAACGAGGTGGGCCATGGGGTGGACTTAATCT	749	
Db	601	CAGATCATTAAGGAGGGCCAGCTTTACCAACGAGGTGGGCCATGGGGTGGACTTAATCT	660	
QY	750	AATTTTACGCTGAAACTCTGGCTGACACAGGTAACTGGGCCCTTTCAAGAGATGCAAAA	809	
Db	661	AATTTTACGCTGAAACTCTGGCTGACACAGGTAACTGGGCCCTTTCAAGAGATGCAAAA	720	
QY	810	TGAATATATCAGATTAATGATGGAAGATGTATCTCCCAAGTCAAAAGATATCAAGCAG	865	

[illegible]

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Db      614 GCCAGACCTTACCCATCAATTTTCAAGACATTAAGCAGACACGCTTTACC 673
Qy      719 AACGGGCTGGGCCATGGGGTGGACCTTAATCATATTTACGGTGAACCTGGCTAGACAG 778
Db      674 AAGGATTTGGGCCATGGGGTGGACCTTAATCATATTTATGGGGAACTTTGGATAGACAA 733
Qy      779 CGTAACTGGGCTTTTCAAGATGGAATAATGAAATTCAGATTAATTTGATGAGACATG 838
Db      734 CATMACTGGGCCCTTTTCAAGATGGAATAATGAAATTAAGATTAATGATGAGAGGTG 793
Qy      839 TATCTCCCAACAGTCAAAAGATTAATCAAGCAGAGATTAATCACTCCCTCAAGTCCCTGAG 898
Db      794 TATCTCTCAACGCTCAAAAGATTAATCAAGTCAAGATTAATCACTCCCTCAAGTCCCTGAG 853
Qy      899 CATCTAGGCTTGTGTGGGGCAGAGAGTCTTGGTCTGTGGTCTGTGTATGATGAT 958
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Qy      959 GCCCAATCTGGCTGGGGGAAACAACAGATTAATGATGATGATGATGATGATGATGATGAT 1018
Db      914 GCCCAATCTGGCTGGGGGAAACAACAGATTAATGATGATGATGATGATGATGATGATGAT 973
Qy      1019 GAATGGGGTGAATGAGACATTTGTTCCAGACAGACAGGCTAATATGATGAGAGACTATT 1078
Db      974 GAATGGGGTGAATGAGACATTTGTTCCAGACAGACAGGCTAATATGATGAGAGACTATT 1033
Qy      1079 AAGATTTGATGAGATTAATGATGAGACATTTGATGAGACATTTGATGAGACATTTGAT 1138
Db      1034 AAGATTTGATGAGATTAATGATGAGACATTTGATGAGACATTTGATGAGACATTTGAT 1093
Qy      1139 GACCCAGACATCTTTTCAACAAATTCAGATTAATGATGAGACATTTGATGAGACATTTGAT 1198
Db      1094 GACCCAGACATCTTTTCAACAAATTCAGATTAATGATGAGACATTTGATGAGACATTTGAT 1153
Qy      1199 AACACCTCTCACTGAGACATTTGTTCCAGACAGACAGGCTAATATGATGAGAGACTATT 1258
Db      1154 AACACCTCTCACTGAGACATTTGTTCCAGACAGACAGGCTAATATGATGAGAGACTATT 1213
Qy      1259 TACAACTATCAACAGTTTATCTTACAACTCTATATGATGAGACATTTGATGAGACATTTGAT 1318
Db      1214 TACAACTATCAACAGTTTATCTTACAACTCTATATGATGAGACATTTGATGAGACATTTGAT 1273
Qy      1319 TTTGTTGATCACTTACACAGGAAATGCTGGCAGAGGTTGCTGGTGAAGAAATGTTCCA 1378
Db      1274 TTTGTTGATCACTTACACAGGAAATGCTGGCAGAGGTTGCTGGTGAAGAAATGTTCCA 1333
Qy      1379 CCGGAGATACAGAAATGATCAAGGCTTCCATTTGACCAAGAGCAGACATGAAATACAG 1438
Db      1334 GCTGAGATACAGAAATGATCAAGGCTTCCATTTGACCAAGAGCAGACATGAAATACAG 1393
Qy      1439 TCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1498
Db      1394 TCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1453
Qy      1499 AAGAGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
Db      1454 AAGAGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1513
Qy      1559 GAGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1618
Db      1514 GAGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1573
Qy      1619 AATGTAAGATGTAAGACATTTCTCTTGAAGAAAGCTTATGGTATATGTTATGTTCT 1678
Db      1574 AATGTAAGATGTAAGACATTTCTCTTGAAGAAAGCTTATGGTATATGTTATGTTCT 1633
Qy      1679 CCGGCTATCTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAAAATCAATCAACACT 1738
Db      1634 CCGGCTATCTGGAAGCAAGCACTTTTGGTGAAGAGTGGGTTTCAAAATCAATCAACACT 1693
Qy      1739 GCCTCAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1798

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Db      1694 GCCTCAATCCAGTCTCTCATCTGCAATTAAGTGAAGGGCTGTCATTCATCTCTCT 1753
Qy      1799 GTTCCAGATCCAGAGCTCATTTTAAACAGTACACATGAATGAGAGTCTCCGCTCCGGA 1858
Db      1754 GTTCCAGAGCTGAGACATCCACCAACCAACAGTACATTAATGAGAGTCTCCGCTCCGGA 1813
Qy      1859 CTAGATATATCAATCCACAGTACTACTTAAAGAAAGCGTGAAGTGAAGTGAAGTGAAGTGA 1918
Db      1814 CTAGATATATCAATCCACAGTACTACTTAAAGAAAGCGTGAAGTGAAGTGAAGTGAAGTGA 1873
Qy      1919 AATGATCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1978
Db      1874 GTTATATCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1930
Qy      1979 TTTATTTAACTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2038
Db      1931 TTTATTTAACTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1966
Qy      2039 CGGAGAAAGAGTCAATCTGTTGAAGACTTTATGTCATCTACTTAAAGATTTGCTGTT 2098
Db      1967 AGGAGAAAGAGGTCATCTGTTGAAGACTTTATGTCATCTACTTAAAGATTTGCTGTT 2021
Qy      2099 GCTGTTAAGTTTGAAGAAAGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2158
Db      2022 TCGGTTTAAAGAGGAAACAGTTT-----TTCTGTTTAAATGAG-----TTT 2065
Qy      2159 GAGCTCTTTTACTGATTTCACTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2215
Db      2066 GAGCTCTTTTACTGATTTCACTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2125
Qy      2216 AATATTTAACTATTCACAAAGATGCAAAATGCTGAAAGTTT-----ACATGTCAT 2271
Db      2216 GATATTTAACTATTCACAAAGATGCAAAATGCTGAAAGTTT-----ACATGTCAT 2185
Qy      2272 GTTTCATGATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2331
Db      2186 ATTTCTATGATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2245
Qy      2332 TTTGGGATTTTCTGTCATCAA 2355
Db      2246 TGTTAGCCACTGTGTGTAGAAA 2269

RESULT 14
US-09-919-060-6/C
; Sequence 6, Application us/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 6
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-6

Query Match      47.9%; Score 1621.6; DB 4; Length 3509;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 314; Indels 55; Gaps 7;
Qy      59 CAAAGCTACCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118
Db      3496 CACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3437
Qy      119 CTGTGGCGGCTCTGCGCTGACCATTAACGAAATCTTGTGTTCCACCATGATGCA 178

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Db 3436 CTCTGCGCGCCCTGGGGGTGTCGCCGCGACGACAAATCTCTGCTGTTCCACCCACTGTCA 3377  
 QY 179 AACGAGGTATGATGATGAGTGTGGATTTGACACATATATAGGTGATGTACCCGAC 238  
 Db 3376 AACCAAGATATTTGTATGACACAGATTTTGAACAATATATAGTGTGACACTGACCGAAC 3317  
 QY 239 GGAATTATGAGAAAACTGCTCAACACCGGAATTTTGCACAGATAATAATTATTTCG 298  
 Db 3316 GGAATTCAGGGCGAAAACTGTCTCAACCGGAATTTTGCACAGATAATAATTATTTCG 3257  
 QY 299 AAACCACTCCAAACACAGTGCATCATATTACCACCTCAAGGATTTTGGAAACGTT 358  
 Db 3256 AAACCACTCCAAATCAGTACATCACTATACCACCTCAAGGAGTCTGGAACATT 3197  
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 Db 3196 GTCAATATACATCCCTCTCTCGGAATATCAATTAAGAAATATGTGTACATCCGGTCA 3137  
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 Db 3076 TTTCTTAACCTCTCCCTATTTATCCAGAGCTTCTCCCTGTACCTGATGACTGTCCAA 3017  
 QY 539 CCTTGGGTGTCAAAAGGTAAAGAGCTTCTCTGATTAATATGAGATTGTGAAAAATTG 598  
 Db 3016 CCGATGGGTGTAAAGAGCAGAAAGAGCTTCTGATTAAGAAAGATTGTGAAAAATTG 2957  
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 QY 1139 GACCCAGAACTACTTTTCAACAAATTCACGATACCAAAATCGTATTTGCTGTGAATTT 1198  
 Db 2416 GACCCAGAGCTGCTTTTCAACCAACATTCACGATACCAAAACGCAATTTGCTGTGAATTT 2357  
 QY 1199 AAGCCCTCTATCATGTGATCCCTTCTGCTGACACTTTCAAAATCATGACCGAA 1258

Db	2356	AACAACACTCTACCACTGGCATCCCTCTCCCTGACCACTTCGTCAAAATGATGACCAAGGAG	2297
QY	1259	TACAACTATCAACAGTTTATCTTACAACAACCTCTATATTGCTGGAAACATGGAAATTTC	1318
Db	2296	TACAAATTTCCAAAGTTTATCTTACAACAACCTCTATATTGTTGAAACAATGGCTTAC	223
QY	1319	TTTGTGTAATCATTCACACGAGCAAAATGCTGACGAGGTGCTGTGTGTAATTTTCCA	1376
Db	2236	TTGTGTGATTCATTGACGAGGCAAAATGTGTGCAAGGTTGCCGTGTGACAGAAATTTCCA	2177
QY	1379	CCCGAGGTACAGAAAGTATCAAGGCTTCATTGACAGAGCAGCAGATGAATACGAG	1438
Db	2176	GCTGACAGTACCAACAGATGACAAACCTTCGATTGACAGACAGACAGATGAATACGAG	2117
QY	1439	TCCTTTAATGAGTACCGCAACGCTTTATNGCTAAGCCCTATGAAATCATTTGAAGACTT	1498
Db	2116	TCTCTTAATGATATCGCAACAGCTTTAAGCTGAAGCCCTTATACATCATTTGAAAGACTT	2057
QY	1499	ACAGAGAAAGAAATGTCTGCAAGTTGGAGACATCTATGGTGACATGATGCTGTG	1558
Db	2056	ACAGAGAGAAAGAAATGGCTGTGGGGTTGAGAGCCCTTATGTGTGATTTGATGCCATG	1997
QY	1559	GAGCTGTATCTCGCCCTTCTGTGTAAGAAAAGCCTGTGGCCAGATGTCATCTTTGTGAACC	1618
Db	1996	GAGCTGTATCTCGCCCTTCTGTGTAAGAAAAGCCTGTGGCCAGATGTCATCTTTGTGAGACC	1937
QY	1619	ATGATAGAAAGTTGAGACCAATTCCTCTGAAAGGACCTATAGGGTAAATGTTATATGTTCT	1678
Db	1936	ATGATAGAAATGGAGACCAATTCCTCTGAAAGGACCTATAGGGTAAATTCCTATGTTCA	1877
QY	1679	CTGCGCTACTGGAAAGCCAAAGCACTTTTGTGTAAGAGTGGGTTTTCAAATCATCAACT	1738
Db	1876	CCTGACTACTGGAAAGCCAGACCTTTGTGTGTAAGAGTGGGTTTTCAAATCATCAACT	1817
QY	1739	GCTCAATTCAGTCTCTATCTGCAATATCGTGAAGGGCTGTCCCTTACTTCATTCAGT	1798
Db	1816	GCTCAATTCAGTCTCTATCTGCAATATCGTGAAGGGCTGTCCCTTACTTCATTCAGT	1757
QY	1799	GTTCCAGATCCAGAGCTCATTAACACGTACCCATCATGCAAGTTCTTCCCGTCCGGA	1858
Db	1756	GTTCCAGAGCGACATCAACCAACACAGTCCATATATGCAAGCTTCTTCCCGTCCGGA	1697
QY	1859	CTAGATGATCAATCCACAGTCTACTTAAAGAACGGTGTGACTGAACGTGAAGTCT	1918
Db	1696	CTAGATGATCAATCCACAGTCTACTTAAAGAACGGTGTGACTGAACGTGAAGTCT	1637
QY	1919	AATGATCATATTTATTTATTTATATGAAACCAATGCTATATATTTATTTATATATAT	1978
Db	1636	GTTATATCTATTTATTTATTTATATGAAACCAATGCTATATATTTATTTATATATAT	1580
QY	1979	TTATATTTAAATCTCTTATGTTACTTAAACCTTCTGTAACAGAAATGACTCTGTG	2038
Db	1579	TTATGTTAAATCTCTTATGTTACTTAAACCTTCTGTTAAATGAG-----TTT	1544
QY	2039	CGAGAAAGAGTCAATCTGTGAAGCTTTATGTCACTACTTAAAGATTTTGCTGT	2098
Db	1543	AGGAGAAAGGGGTATCTGTGTGAAGTTTTCATGTCACTATTTTAAAGTGT-----CT	1489
QY	2099	GCTGTAAAGTTGGAAAACAGTTTATTTATCTGTGTTTATAAACCAAGAGAAATGAGTTT	2158
Db	1488	TCCGGGTAAAGAGAAAACAGTT-----TTCGTGTTTATTAATGAG-----TTT	1445
QY	2159	GAGCTCTTTTATCTGTAATTTCAACTATATTTATATGAGACGAAAGTAA--AGATGTTTG	2215
Db	1444	GACATCTCTTATCTGTAATTTCAACTATATTTATATGAGACGAAAGATGTTG	1385
QY	2216	AATACCTTAAACATATCAACAAGATGCCAAATGCTGAAGTTT-----ACACTGTGCAT	2271
Db	1384	GATATTTAAATGCTGTCCAGATGACAAAAATGCTGCAGTTTTCGACACTATGCGG	1325
QY	2272	GTTTCCATGATCTTCATGATGACATTTGAAGTAACTATATGTTGAAATTTTAAAGTAC	2331
Db	1324	ATTTCATGATCTTCCTCGAGCTTGAAGCACTCTGACACATTTCTTTTCTTC	1265

QY 2332 TTTGGGTATTTTCTGTCAATCAA 2355  
 Db 1264 TGTTAGCCACTGTGTGTGTAGAAA 1241

## RESULT 15

US-08-627-254C-27  
 ; Sequence 27, Application US/08627254C  
 ; Patent No. 5859229

## GENERAL INFORMATION:

APPLICANT: Kniss, Douglas A.  
 TITLE OF INVENTION: Eicosanoid Formation  
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calfee, Halter & Griwold LLP  
 STREET: 800 Superior Avenue  
 CITY: Cleveland  
 STATE: Ohio  
 COUNTRY: USA

ZIP: 44114  
 COUNTRY: USA

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/627,254C  
 FILING DATE:

CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:

NAME: Golrick, Mary E  
 REGISTRATION NUMBER: 34,829  
 REFERENCE/DOCKET NUMBER: 18525/00107

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (216) 622-8200  
 TELEFAX: (216) 241-0816

INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3986 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHEITICAL: NO  
 ANTI-SENSE: NO

US-08-627-254C-27

Query Match 45.0%; Score 1525.8; DB 2; Length 3986;

Best Local Similarity 76.6%; Pred. No. 0;  
 Matches 2048; Conservative 0; Mismatches 582; Indels 43; Gaps 13;

QY 69 CCCCCGCGCGCCCTGCGCGCGCGCTGCGATGCTGCGCGCGCCCTGCTGCTGCGCGG 128  
 Db 96 CCACGTGCACCTCCGCTGCGACCTCTGCGATGCTCTTCGAGCTGTGCTGCTGCGCTG 155  
 QY 129 TCCTGCGCTGACGCTATACAGCAATCTCTGCTGTTCCACCCAGCTCAAAACGAGGTG 188  
 Db 156 CCTCTGCGCTGACGAGGAGCAAAATCTTGTGTTCCATCATCTCAAAACCGTGGGG 215  
 QY 169 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 248  
 Db 216 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 275  
 QY 249 GAGAAAACTGCTCAACCCGGAATTTTTCAGAAATTAATTAATTTCTGAAACCCACTC 308  
 Db 276 GGGAAAACTGCTCAACCCGGAATTTTTCAGAAATTAATTAATTTCTGAAACCCACTC 335  
 QY 309 CAAACAGCTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 368  
 Db 336 CAAACAGCTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 395  
 QY 369 TTCCCTCTCTGGAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 428

Db 396 TCCCTCTCTCTGGAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 455  
 QY 429 ACACTCCACCACTTACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 488  
 Db 456 ACACTCCACCACTTACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 515  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 11:20:32 ; Search time 1301 Seconds

(without alignments)  
11737.678 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387  
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Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3379	99.8	3387	16	US-10-191-997-87 Sequence 87, Appl
2	3374.2	99.6	3387	15	US-10-027-961A-19 Sequence 19, Appl
3	3216.6	95.0	4465	10	US-09-953-067A-2 Sequence 2, Appl
4	3216.6	95.0	4465	13	US-10-211-462-132 Sequence 132, Appl
5	3216.6	95.0	4465	13	US-10-170-385-238 Sequence 238, Appl
6	3216.6	95.0	4465	15	US-10-021-660-42 Sequence 42, Appl
7	3216.6	95.0	4465	16	US-10-295-027-31 Sequence 31, Appl
8	3216.6	95.0	4465	16	US-10-373-801-11 Sequence 11, Appl
9	3215	94.9	4496	14	US-10-044-090-478 Sequence 478, Appl
10	3215	94.9	4496	14	US-10-071-766-46 Sequence 46, Appl
11	3215	94.9	4750	15	US-10-247-671-126 Sequence 126, Appl
12	2513.4	74.2	2563	14	US-10-044-090-477 Sequence 477, Appl
13	1727	51.0	9453	9	US-09-954-456-324 Sequence 324, Appl
14	1717.4	50.7	11064	10	US-09-949-293-25 Sequence 25, Appl

15	1621.6	47.9	3509	9	US-09-919-060-4	Sequence 4, Appl
16	1621.6	47.9	3509	9	US-09-919-060-6	Sequence 6, Appl
17	1525.8	45.0	3986	10	US-09-953-067A-6	Sequence 7, Appl
18	1476.6	43.6	1812	9	US-09-919-060-7	Sequence 8, Appl
19	1476.6	43.6	1812	9	US-09-919-060-8	Sequence 103, Appl
20	1431.8	42.3	4404	16	US-10-191-803-103	Sequence 13, Appl
21	727.6	21.5	1807	13	US-10-382-248-5	Sequence 5, Appl
22	727.6	21.5	1894	16	US-10-260-937-13	Sequence 229, Appl
23	727.6	21.5	2554	9	US-09-962-832-229	Sequence 1, Appl
24	727.6	21.5	2554	10	US-09-953-067A-1	Sequence 263, Appl
25	727.6	21.5	2554	15	US-10-097-340-263	Sequence 167, Appl
26	727.6	21.5	5049	14	US-09-971-392-167	Sequence 327, Appl
27	727.6	21.5	5049	14	US-10-044-090-327	Sequence 12, Appl
28	724.4	21.4	1894	16	US-10-260-937-10	Sequence 3, Appl
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30	713	21.1	2757	10	US-09-953-067A-5	Sequence 11, Appl
31	705.2	20.8	1902	16	US-10-260-937-1	Sequence 1, Appl
32	705.2	20.8	2706	16	US-10-260-937-3	Sequence 15, Appl
33	703.6	20.8	1899	9	US-09-919-060-15	Sequence 16, Appl
34	703.6	20.8	1899	9	US-09-919-060-16	Sequence 12, Appl
35	703.6	20.8	2693	9	US-09-919-060-12	Sequence 57, Appl
36	703.6	20.8	2693	9	US-09-919-060-14	Sequence 7, Appl
37	702	20.7	2587	16	US-10-260-937-55	Sequence 14, Appl
38	689.6	20.4	2682	16	US-10-260-937-57	Sequence 15, Appl
39	597.4	17.6	1713	13	US-10-382-248-7	Sequence 9708, Appl
40	552.8	16.3	574	15	US-10-029-386-9708	Sequence 168, Appl
41	552	15.4	2329	16	US-09-971-392-168	Sequence 12, Appl
42	523.2	15.4	1746	10	US-10-260-937-12	Sequence 21077, A
43	440	13.0	493	9	US-09-918-995-21077	Sequence 1, Appl
44	422.6	12.5	542	9	US-09-919-060-1	Sequence 3, Appl
45	422.6	12.5	542	9	US-09-919-060-3	

## ALIGNMENTS

RESULT 1  
US-10-191-997-87  
Sequence 87, Application US/10191997  
Publication No. US20030207834A1  
GENERAL INFORMATION:  
APPLICANT: Oligos Etc., Inc.  
APPLICANT: DALE, Roderic M. K.  
APPLICANT: ARROW, Amy  
APPLICANT: THOMPSON, Terry  
TITLE OR INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their  
FILE REFERENCE: 54800-5019  
CURRENT APPLICATION NUMBER: US/10/191,997  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US 60/303,820  
PRIOR FILING DATE: 2001-07-10  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 87  
LENGTH: 3387  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Cox2: Acc. No. US20030207834A1 M90100  
US-10-191-997-87  
Query Match 99.8%; Score 3379; DB 16; Length 3387;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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Matches 3310;	Conservative	0;	Mismatches 59;	Indels 18; Gaps 4;

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Db	158	GTGCGCGGTTCTGGGCGCTCAGCCCATACAGCAAAATCCTGTCGTTCACCCCATGTCAAAA	217
QY	181	CCGAGGTGATATATAGAGTGGAGTTTACCAAGTATAGTGCATTGATCCCGACAG	240
Db	218	CCGAGGTGATATATAGAGTGGAGTTTACCAAGTATAGTGCATTGATCCCGACAG	277
QY	241	ATTCTATGAGAAAACTGCTCAACCCGGAAATTTTGAACAAGATTAATTTATCTGAA	300
Db	278	ATTCTATGAGAAAACTGCTCAACCCGGAAATTTTGAACAAGATTAATTTATCTGAA	337
QY	301	ACCCACTCCAAACACAGTGCATACATCTTACCACTTCAAGGATTTTGGACGTTGT	360
Db	338	ACCCACTCCAAACACAGTGCATACATCTTACCACTTCAAGGATTTTGGACGTTGT	397
QY	361	GAATTAACATTCCTCTCTTCCAAAAGCATTTATGATATGTGTGACATCCAGATCACA	420
Db	398	GAATTAACATTCCTCTCTTCCAAAAGCATTTATGATATGTGTGACATCCAGATCACA	457
QY	421	TTTGATTTGACAGTCCACCACTTACAAATGCTACATATGGCTTCAAAAGCTGGGAAGCCT	480
Db	458	TTTGATTTGACAGTCCACCACTTACAAATGCTACATATGGCTTCAAAAGCTGGGAAGCCT	517
QY	481	CTTAACTCTCTTATTTATCTAGAGCCCTCTCTGCTGCTGATGATTTGCCCATCC	540
Db	518	CTTAACTCTCTTATTTATCTAGAGCCCTCTCTGCTGCTGATGATTTGCCCATCC	577
QY	541	CTTGGGTGTCAAAGGTATAAAAGACGCTTCTGATTTCAATAGATTTGGAAAAATTGCT	600
Db	578	CTTGGGTGTCAAAGGTATAAAAGACGCTTCTGATTTCAATAGATTTGGAAAAATTGCT	637
QY	601	TCTAAGAGAAAGTTCAATCCCTGATATCCCAAGGCTCAAAACATGATGTTTGACTTCTTGC	660
Db	638	TCTAAGAGAAAGTTCAATCCCTGATATCCCAAGGCTCAAAACATGATGTTTGACTTCTTGC	697
QY	661	CCAGCACTTCCAGCACAGATTTTTCAAACACAGATCATTAAGGAGGGCAGCTTCAACAA	720
Db	698	CCAGCACTTCCAGCACAGATTTTTCAAACACAGATCATTAAGGAGGGCAGCTTCAACAA	757
QY	721	CGGCTGGGCGCATGGGCTGGACTTAATCATATTTACGGTGAACCTCGGCTAGACAGCG	780
Db	758	CGGCTGGGCGCATGGGCTGGACTTAATCATATTTACGGTGAACCTCGGCTAGACAGCG	817
QY	781	TAAACTGGGCTTTTTCAAAGATGGAATAATGAATATCAGATTAATTGATGGAGAGATGTA	840
Db	818	TAAACTGGGCTTTTTCAAAGATGGAATAATGAATATCAGATTAATTGATGGAGAGATGTA	877
QY	841	TCTCTCCACAGTCAAAAGTACTCAGGACAGAGATGATCTAACCTCTCAAGTCCCTGAGCA	900
Db	878	TCTCTCCACAGTCAAAAGTACTCAGGACAGAGATGATCTAACCTCTCAAGTCCCTGAGCA	937
QY	901	TCTACGGTTTCTGTGGGACAGAGGCTTGTGTGCTGGTGCCTGCTGATGATGTATGC	960
Db	938	TCTACGGTTTCTGTGGGACAGAGGCTTGTGTGCTGGTGCCTGCTGATGATGTATGC	997
QY	961	CACAACTGGGTGGGGGAAACAACAAGATATGTGATGTGCTTTAAACAGAGCATCTCTGA	1020
Db	998	CACAACTGGGTGGGGGAAACAACAAGATATGTGATGTGCTTTAAACAGAGCATCTCTGA	1057
QY	1021	ATGGGTTGATCAGCAGTTGTTCCAGACAGACGCTATATCTGATAGAGAGCATATTTAA	1080
Db	1058	ATGGGTTGATCAGCAGTTGTTCCAGACAGACGCTATATCTGATAGAGAGCATATTTAA	1117
QY	1081	GATTTCATGAAAGATTATGTGCAACACTTGAGTGGCTATCATCTTCAACTGAATTTTGA	1140

Db	1118	GATTGCGATTGAAGATTATGTGAAACACTTGAGTGGCTATCACTTCAAACTGAAATTTGA	1177
QY	1141	CCGAGAACTACCTTTCCACAAACAATTCGATACAAAATCGTATTGCTGCTGAATTTAA	1200
Db	1178	CCGAGAACTACTTTTCAACAAACAATCCAGTACCAAAATCGTATTGCTGCTGAATTTAA	1237
QY	1201	CACCCCTATACAGTGGCATCCCTCTCGGCTGACACCTTTCAAATTCATGACAGAAATTA	1260
Db	1238	CACCCTCTATACAGTGGCATCCCTCTCGGCTGACACCTTTCAAATTCATGACAGAAATTA	1297
QY	1261	CAACTATCAACAGTTTATCTACAAACAACCTCATATTGCTGGAAACATGSAATTA	1320
Db	1298	CAACTATCAACAGTTTATCTACAAACAACCTCATATTGCTGGAAACATGSAATTA	1357
QY	1321	TGTTGAATTCATTCACGAGCAAAATGCTGGCAGGGTTCCTGGTGTGTAGAAATGTTCCAC	1380
Db	1358	TGTTGAATTCATTCACGAGCAAAATGCTGGCAGGGTTCCTGGTGTGTAGAAATGTTCCAC	1417
QY	1381	CGCAGTACAGAAAGTATCACAGGCTTCCATTTGACACAGACAGGACAGTAAATACAGTTC	1440
Db	1418	CGCAGTACAGAAAGTATCACAGGCTTCCATTTGACACAGACAGGACAGTAAATACAGTTC	1477
QY	1441	TTTTTATGAGTACCGCAAAAGCGTTTATGTGTAAGCCCTATGATCATTTTGAAGACTTAC	1500
Db	1478	TTTTTATGAGTACCGCAAAAGCGTTTATGTGTAAGCCCTATGATCATTTTGAAGACTTAC	1537
QY	1501	AGGAGAAAAGAAATGTCTGCAAGTGTGGAAGCACTCTATGTGTACATTCGATGCTGTGGA	1560
Db	1538	AGGAGAAAAGAAATGTCTGCAAGTGTGGAAGCACTCTATGTGTACATTCGATGCTGTGGA	1597
QY	1561	GCTGTATCTGCGCCCTTCTGTGTAAGAAAGCCTGGCCAGATGCCATCTTTGTGTGAACCAT	1620
Db	1598	GCTGTATCTGCGCCCTTCTGTGTAAGAAAGCCTGGCCAGATGCCATCTTTGTGTGAACCAT	1657
QY	1621	GGTGAAGTGTGACACCACTTCTCCCTTGAAAGACCTTAATGGGTAAATGTATATGTTCC	1680
Db	1658	GGTGAAGTGTGACACCACTTCTCCCTTGAAAGACCTTAATGGGTAAATGTATATGTTCC	1717
QY	1681	TGCCCTACTGGAAGCAAGCACTTTTGGTGTGAGAAAGTGGGTTTTCAATTCATCAACATGCG	1740
Db	1718	TGCCCTACTGGAAGCAAGCACTTTTGGTGTGAGAAAGTGGGTTTTCAATTCATCAACATGCG	1777
QY	1741	CTCAATTCAGTCTCTCATCTGCAATTAACGTGTGAAGGGCTGTCCCTTTACTTCATTCAGTGT	1800
Db	1778	CTCAATTCAGTCTCTCATCTGCAATTAACGTGTGAAGGGCTGTCCCTTTACTTCATTCAGTGT	1837
QY	1801	TCCAGATCCAGAGCTCATTTAAACAGTCAACCATCAATGCAAGCTCTCCCGCTCCGAGCT	1860
Db	1838	TCCAGATCCAGAGCTCATTTAAACAGTCAACCATCAATGCAAGCTCTCCCGCTCCGAGCT	1897
QY	1861	AGATGATATCAATCCCAACAAGTACTCTAATAAGAACGCTGCACTGAACCTGTGAAGTCTTAA	1920
Db	1898	AGATGATATCAATCCCAACAAGTACTCTAATAAGAACGCTGCACTGAAGTCTTAA	1957
QY	1921	TGATCATATTTAATTTAATTAATGACACACATCATTAATTAATTTAATTAATTAATTT	1980
Db	1958	TGATCATATTTAATTTAATTAATGACACACATCATTAATTTAATTTAATTTAATTAATTT	2017
QY	1981	ATATTTAACTCCTTATGTACTTTAACATCTTCTGTGAACAGAGTCACTCTCGTTGCG	2040
Db	2018	ATATTTAACTCCTTATGTACTTTAACATCTTCTGTGAACAGAGTCACTCTCGTTGCG	2077
QY	2041	GAGAAAGAGTCAATCTGTGAAAGCTTTTATGTCACTACCTTAAGATTTTGTGCTGGC	2100
Db	2078	GAGAAAGAGTCAATCTGTGAAAGCTTTTATGTCACTACCTTAAGATTTTGTGCTGGC	2137
QY	2101	TGTTAAGTTTGGAAAAAGTTTATATCTGTTTATTAATAACAGACAGAAATGAGTTTGA	2160
Db	2138	TGTTAAGTTTGGAAAAAGTTTATATCTGTTTATTAATAACAGACAGAAATGAGTTTGA	2197
QY	2161	CGTCTTTTACTGAAATTTCAACTTATATTAAGACGAAAGTAAAGATGTTTGAATAC	2220

Db	2198	CGCTCTTTTACTGGAAATTTCAACTTAAATTAATAGAACCAAGGAATGAAGTGTGAATAC	2255
OY	2221	TTAAACGCTTACCAAGATGCCAAATATGCTGAAGATTTTTTACACGTGCATGTTTCCAA	2280
Db	2258	TTAAACCATACACAGATGGCAAAAATGCTGAAGATTTTTTACACGTGCATGTTTCCAA	2317
OY	2281	GCATCTTCCATGATGCAATTAGAACTAAATGTTGAAATTTTAAAGTACTTTGGGTA	2340
Db	2318	GCATCTTCCATGATGCAATTAGAACTAAATGTTGAAATTTTAAAGTACTTTGGGTA	2377
OY	2341	TTTTTCGTGATCAAC-AAAACAGGTATCAGTGCATTTAATGCAATTTTAAATTTAG	2399
Db	2378	TTTTTCGTGATCAACAAACAAACAGGTATCAGTGCATTTAATGCAATTTTAAATTTAG	2437
OY	2400	ACATTACAGTAATTTTATGTCATCTTCTTAAATATGCAATGAAACAAATATTTGAAAT	2459
Db	2438	ACATTACAGTAATTTTATGTCATCTTCTTAAATATGCAATGAAACAAATATTTGAAAT	2497
OY	2460	TTCTAAATTCATAGGGTAGAATCACTGTAAGAGCTTGTTGATTTCTTAAAGTATTTAA	2519
Db	2498	TTCTAAATTCATAGGGTAGAATCACTGTAAGAGCTTGTTGATTTCTTAAAGTATTTAA	2557
OY	2520	ACTTGCATATACCAAAAAGAGCTGCTGGATTTAAATCTGTAATCAATGCAATGAAT	2579
Db	2558	ACTTGCATATATCCAAAAAGAGCTGCTGGATTTAAATCTGTAATCAATGCAATGAAT	2617
OY	2580	TTTATCTACAAATGCTGTAAATATTTTAAATGATGATGTTCTTTTCAACCAAGTAT	2639
Db	2618	TTTATCTACAAATGCTGTAAATATTTTAAATGATGATGTTCTTTTCAACCAAGTAT	2677
OY	2640	AAACCTTTAAGTGTGACGTGTAATAATCTCCTTTAAATCAAAATGCAATTTATTAAG	2699
Db	2678	AAACCTTTAAGTGTGACGTGTAATAATCTCCTTTAAATCAAAATGCAATTTATTAAG	2737
OY	2700	GTGGTGAGGCACATGCAAGTGTATCTTCAAAATAGAAATATCTGTGAGATTTCCAGAA	2759
Db	2738	GTGGTGAGGCACATGCAAGTGTATCTTCAAAATAGAAATATTTGTGAGATTTCCAGAA	2797
OY	2760	TCTGTATTATAGGTGTGTAACATGTAAACCCCATACCCCGCAAAAGGGGTCCAC	2819
Db	2798	TTTGTATTATAGGTGTGTAACATGTAAACCTCTATATAGC-----AAAAGGTCTAC	2850
OY	2820	CTTGAACATTAAGCAATATACCAAGAGAAAGCCCAATTTATGTTCCAAATTTAGGG	2879
Db	2851	TTTAA-----AATAGCAATTAAGAGAGAAACCAATTTATGTTCCAAATTTAG	2901
OY	2880	TTTAACTTTTGAAGCAACTTTTTTTTTAGCCTTGTCACCTGCAACCTTGTAATCTAGA	2939
Db	2902	GTTTAACTTTTGAAGCAACTTTTTTTTTATCTCTTGCACTGAGGCTGTGTAATCTAGA	2961
OY	2940	TTTGTGATAGAGTTAATGAAGTGCACCAAGCTGTGTAATGAATGTTTCTAGA	2999
Db	2962	TTTGTGATAGAGTTAATGAAGTGCACCAAGCTGTGTAATGAATGTTTCTAGA	3021
OY	3000	TTTTCTGTGTACAGTTTAATTTAGCAAGTCCATATCAATTGCAAAAGTACGAATGACT	3059
Db	3022	TTTTCTGTGTACAGTTTAATTTAGCAAGTCCATATCAATTGCAAAAGTACGAATGACT	3081
OY	3060	CATATAAATCTCTTCAAAATGCTAAATCATTTCACTACATTAATTTTATCTAGCTT	3119
Db	3082	CATATAAATCTCTTCAAAATGCTAAATCATTTCACTACATTAATTTTATCTAGCTT	3141
OY	3120	GAAGCAATTCAGTAGTGTGATGGAAATCAAGCTGTGCTACTGCAATGCTGTTCTTTTC	3179
Db	3142	GAAGCAATTCAGTAGTGTGATGGAAATCAAGCTGTGCTACTGCAATGCTGTTCTTTTC	3201
OY	3180	TTTTCTTCTTTAGCCATTTTGTATAGAGACAGTCTTCTCAACCACTTGCTTCTCCT	3239
Db	3202	TTTTCTTCTTTAGCCATTTTGTATAGAGACAGTCTTCTC-ACTGTTCTTCTCCT	3260
OY	3240	AATTTGTTTACTAATTTTAAAGTACAGTGTCACTTTTGTGAAGCTGACCTATATTTTC	3299
Db	3261	AATTTGTTTACTAATTTTAAAGTACAGTGTCACTTTTGTGAAGCTGACCTATATTTTC	3320

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QY 3300 TTACCGAAGCTTTTGGAGTTTTCAGCTAAACCTCAGCTCAGCTGCTATTAGTCTCT 3359
DB 3321 TTACCGAAGCTTTTGGAGTTTTCAGCTAAACCTCAGCTCAGCTGCTATTAGTCTCT 3380
QY 3360 CTTAAGAGATTAAAAA 3386
DB 3381 CTTAAGAGATTAAAAA 3407

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RESULT 4
US-10-211-462-132
; Sequence 132, Application US/10211462
; Publication No. US2004003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 4465
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-462-132

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Query Match      95.0%; Score 3216.6; DB 13; Length 4465;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 3310; Conservative 0; Mismatches 59; Indels 18; Gaps 4;

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QY 1 GTCCAGAACTCTCTCAGCAGCGCTCTTCACTCACTCAGCAGCAGCCCTCAGACGCA 60
DB 38 GTCCAGAACTCTCTCAGCAGCGCTCTTCACTCACTCAGCAGCAGCCCTCAGACGCA 97
QY 61 AAGCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 120
DB 98 AAGCTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 157
QY 121 GTGCGCGCTCTGCGCGCTCAGCCATAGACCAATCCCTGCTCCCAACCCATGTCAAA 180
DB 158 GTGCGCGCTCTGCGCGCTCAGCCATAGACCAATCCCTGCTCCCAACCCATGTCAAA 217
QY 181 CCGAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 218 CCGAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 277
QY 241 ATTCTATGAGAAAAGTCTCAACACCGGAATTTTGGACAAGAAATTAATTTTGGAA 300
DB 278 ATTCTATGAGAAAAGTCTCAACACCGGAATTTTGGACAAGAAATTAATTTTGGAA 337
QY 301 ACCCACTCCAAACAGTGCATTAACAATTAACCACTTAAGAGATTTTGGAACTTTGT 360
DB 338 ACCCACTCCAAACAGTGCATTAACAATTAACCACTTAAGAGATTTTGGAACTTTGT 397
QY 361 GAATTAACATTCCTCTCTGGAATGCAATTAATGATGATGATGATGATGATGATGATG 420
DB 398 GAATTAACATTCCTCTCTGGAATGCAATTAATGATGATGATGATGATGATGATGATG 457

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QY 421 TTGATGACAGTCCACCACTTAATGCTGATGCTAAGGCTAAGAAAGCTGGAAAGCTT 480
DB 458 TTGATGACAGTCCACCACTTAATGCTGATGCTAAGGCTAAGAAAGCTGGAAAGCTT 517
QY 481 CTCTAACCTCTCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 518 CTCTAACCTCTCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 577
QY 541 CTTGGGTGCAAAAGTAAAGGACGCTTCTGATTAATGATGATGATGATGATGATGATG 600
DB 578 CTTGGGTGCAAAAGTAAAGGACGCTTCTGATTAATGATGATGATGATGATGATGATG 637
QY 601 TCTAAGAGAAAGTTCATCCCTGATCCCAAGGCTCAAAATGATGATGATGATGATGATG 660
DB 638 TCTAAGAGAAAGTTCATCCCTGATCCCAAGGCTCAAAATGATGATGATGATGATGATG 697
QY 661 CCAAGACTTCAAGCAGCTTTTCAAGACAGATCAATAGAGAGAGGAGGCTTCAACAA 720
DB 698 CCAAGACTTCAAGCAGCTTTTCAAGACAGATCAATAGAGAGAGGAGGCTTCAACAA 757
QY 721 CGGCTGGGCGATGGGGTGGACTTAAATCATATTTACGTTAAACTCTGGCTAGACAGCG 780
DB 758 CGGCTGGGCGATGGGGTGGACTTAAATCATATTTACGTTAAACTCTGGCTAGACAGCG 817
QY 781 TAACTGGGCTTTTCAAGAGATGAGAAATGAATATGATGATGATGATGATGATGATG 840
DB 818 TAACTGGGCTTTTCAAGAGATGAGAAATGAATATGATGATGATGATGATGATGATG 877
QY 841 TCTTCCCAAGTCAAAAGTATCTCAGCAGAGATGATCACTCCCTCAAGTCCCTGAGCA 900
DB 878 TCTTCCCAAGTCAAAAGTATCTCAGCAGAGATGATCACTCCCTCAAGTCCCTGAGCA 937
QY 901 TCTAAGGTTTGTGTTGGGGGAGAGGCTTTGATGATGATGATGATGATGATGATGATG 960
DB 938 TCTAAGGTTTGTGTTGGGGGAGAGGCTTTGATGATGATGATGATGATGATGATGATG 997
QY 961 CACATCTGCTGGGGAACAACAGAGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 998 CACATCTGCTGGGGAACAACAGAGATGATGATGATGATGATGATGATGATGATGATG 1057
QY 1021 ATGGGTTGATGAGAGTTGTTCCAGACAGAGCTAATCTGATAGAGAGATTAATTA 1080
DB 1058 ATGGGTTGATGAGAGTTGTTCCAGACAGAGCTAATCTGATAGAGAGATTAATTA 1117
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DB 1118 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1177
QY 1141 CCGAAGTACTTTTCAACAAACATTCAGTACCAAAATCGTATGCTGCTGAATTTAA 1200
DB 1178 CCGAAGTACTTTTCAACAAACATTCAGTACCAAAATCGTATGCTGCTGAATTTAA 1237
QY 1201 CACCTCTATCAGTGGGATCCCTTCTGCTGACACCTTCAAAATTCATGACCAAGATA 1260
DB 1238 CACCTCTATCAGTGGGATCCCTTCTGCTGACACCTTCAAAATTCATGACCAAGATA 1297
QY 1261 CAACATCAACAACTTTATCAACAACTTATATGCTGGAACATGGAATTAACAGTT 1320
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DB 1358 TGTGATCACTTACACAGGCAATGCTGGCAGGGTGTGCTGATGAGAAATGTCACAC 1417
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DB 1418 CGCAGTACAGAAAGTATCAAGGCTTTCATTTGACAGAGCAGAGTGAATACAGTGC 1477
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DB 1478 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1537
QY 1501 AGGAGAAAAGAAATGCTGACAGAGTTGGAAGCCTATGATGATGATGATGATGATG 1560

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Db 1538 AGGAGAAAGAAATGCTGAGAGTGGAGACCTGATGGTACATCGATGCTGGGA 1597  
Qy 1561 GCTGTATCTGCTCCCTTGAGTAAAGCCCTGGCCAGATGCCATCTTGGTGAACCAT 1620  
Db 1598 GCTGTATCTGCTCCCTTGAGTAAAGCCCTGGCCAGATGCCATCTTGGTGAACCAT 1657  
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Qy 1681 TGCCCTACGGAAGCCAGACCTTTGGTGGAGAGTGGGTTTCAAAATCATCAACCTGC 1740  
Db 1718 TGCCCTACGGAAGCCAGACCTTTGGTGGAGAGTGGGTTTCAAAATCATCAACCTGC 1777  
Qy 1741 CTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTACTTCATTCAGTGT 1800  
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Db 1838 TCCGATTCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTTCTCCGCTCCGACT 1897  
Qy 1861 AGATGATATCAATCCCAAGTACTACTPAAGAAAGGCTGCACTGAACTGTAAGTCTAA 1920  
Db 1898 AGATGATATCAATCCCAAGTACTACTPAAGAAAGGCTGCACTGAACTGTAAGTCTAA 1957  
Qy 1921 TGATCAATTTATTTATTAATGAAGCATGTCTATTAATTTATTTATTAATAATTT 1980  
Db 1958 TGATCAATTTATTTATTAATGAAGCATGTCTATTAATTTATTTATTAATAATTT 2017  
Qy 1981 ATATTAACCTCCTTAATGTTACTTAACATCTCTGTAACAGAGTACCTGCTGGCG 2040  
Db 2018 ATATTAACCTCCTTAATGTTACTTAACATCTCTGTAACAGAGTACCTGCTGGCG 2077  
Qy 2041 GAGAAAGAGTCAATCTGTGAGAGCTTTATGTCATCTACTTAAGATTTTGTCTGTC 2100  
Db 2078 GAGAAAGAGTCAATCTGTGAGAGCTTTATGTCATCTACTTAAGATTTTGTCTGTC 2137  
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Qy 2460 TTCTAAATTCATAGGTAGATATCACTGTAAAGCTTTGTTGATTTCTTAAATTTAA 2519  
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Qy 2520 ACTTGACATATATCAAAAGAGAGCTGCTGGATTTAATCTGPAATTCAGATGAAT 2579  
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Qy 2580 TTTACTACATTCCTTGTAAATATTTTAAAGTATGCTCTTTTCAACAGAGTAT 2639

Db 2618 TTTACTACATTCCTTGTAAATATTTTAAAGTATGTTCTTTTCAACAGAGTAT 2677  
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Db 2678 AAACCTTTTATGATGATCTGTAAATCTTCTTTTAAATGAATATGCAATTTATTAAG 2737  
Qy 2700 GTGGTGAAGCCATGCACTGATGTTATCTCAAAATTAAGATATCTGTTAGATTTCCAGAA 2759  
Db 2738 GTGGTGAAGCCATGCACTGATGTTATCTCAAAATTAAGATATTTGTTAGATTTCCAGAA 2797  
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Qy 2880 TTTAACTTTTGAAGCAACTTTTATGCTTGTGCACTGCAAGCTGTGATCTAGA 2939  
Db 2902 GTTTAACTTTTGAAGCAACTTTTATGCTTGTGCACTGCAAGCTGTGATCTAGA 2961  
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Db 3022 TTTTCTGTTGATAGTTAATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3081  
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Db 3142 GAAGCCATTCAGTATGATGATTTGAATCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3201  
Qy 3180 TTTTCTGTTTGAAGTATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3239  
Db 3202 TTTTCTGTTTGAAGTATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3260  
Qy 3240 ATTTGTTTGAAGTATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3299  
Db 3261 ATTTGTTTGAAGTATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3320  
Qy 3300 TTAACCTGATCTTGAAGTATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3359  
Db 3321 TTAACCTGATCTTGAAGTATTTTGAAGTACCAAGCTGTGCTTGAATATGATATGTTTCTAGA 3380  
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Db 3381 CTTAAGAGATTTAAAAAAGAAAAA 3407

RESULT 5  
US-10-170-385-238  
; Sequence 238, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Naylor, Stuart  
; APPLICANT: Kingsman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385



; CURRENT FILING DATE: 2002-06-12  
 ; PRIOR APPLICATION NUMBER: PCT/GB02/01662  
 ; PRIOR FILING DATE: 2002-04-08  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/05458  
 ; PRIOR FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 549  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 238  
 ; LENGTH: 4465  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; US-10-170-385-238

Query Match 95.0%; Score 3216.6; DB 13; Length 4465;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 3310; Conservative 0; Mismatches 59; Indels 18; Gaps 4;

QY	1	GTCCAGAACTCCTCAGCAGCGCTCTCCAGCTCCACAGCAGCGCCCTCAGACAGA	60
DB	38	GTCCAGAACTCCTCAGCAGCGCTCTCCAGCTCCACAGCAGCGCCCTCAGACAGA	97
QY	61	AAGCTACCCCGCGCGCGCGCTCCGCGCTGCGATGCTGCGCGCGCGCTGCTGCT	120
DB	98	AAGCTACCCCGCGCGCGCGCTCCGCGCTGCGATGCTGCGCGCGCGCTGCTGCT	157
QY	121	GTGCGCGCTGCTGCGCGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	180
DB	158	GTGCGCGCTGCTGCGCGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	217
QY	181	CCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	240
DB	218	CCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	277
QY	241	ATTCTATGAG	300
DB	278	ATTCTATGAG	337
QY	301	ACCAGCTCCAAACAGTGCATCATCTTACCACTTCAAGGATTTTGAACGTTGT	360
DB	338	ACCAGCTCCAAACAGTGCATCATCTTACCACTTCAAGGATTTTGAACGTTGT	397
QY	361	GAATTAACATTCCTCTCTCTGGAATGCAATTAAGTATGATGATGATGATGATG	420
DB	398	GAATTAACATTCCTCTCTCTGGAATGCAATTAAGTATGATGATGATGATGATG	457
QY	421	TTTGATGACAGTCCACCACTTAACATGCTGATGCTGATGCTGATGCTGATGCT	480
DB	458	TTTGATGACAGTCCACCACTTAACATGCTGATGCTGATGCTGATGCTGATGCT	517
QY	481	CTCTAACCT	540
DB	518	CTCTAACCT	577
QY	541	CTTGAGGTGTCAGAGTAAAGAGAGCTCTGATTTCAAGATGAAATGGAATTTGCT	600
DB	578	CTTGAGGTGTCAGAGTAAAGAGAGCTCTGATTTCAAGATGAAATGGAATTTGCT	637
QY	601	TCTAAGAGAGAGTTCATCCCTGATCCCAAGGCTCAACATGATGTTGCTTTGCT	660
DB	638	TCTAAGAGAGAGTTCATCCCTGATCCCAAGGCTCAACATGATGTTGCTTTGCT	697
QY	661	CCAGCACTTCAGCAGCAGCTTTTCAAGAGATCATTAAGCGAGGCGCAGCTTTC	720
DB	698	CCAGCACTTCAGCAGCAGCTTTTCAAGAGATCATTAAGCGAGGCGCAGCTTTC	757
QY	721	CGGCGTGGGCGAGTGGGCGAGCTTAATATATTTAOGGGAACCTGGCTGAGAGG	780
DB	758	CGGCGTGGGCGAGTGGGCGAGCTTAATATATTTAOGGGAACCTGGCTGAGAGG	817
QY	781	TAAACTGCGCTTTTCAAGAGTGAAGAAATGAATATCAGATTAATGATGAGAGAT	840
DB	818	TAAACTGCGCTTTTCAAGAGTGAAGAAATGAATATCAGATTAATGATGAGAGAT	877

QY	841	TCTCCCAACAGTCAAGATTAATCAGCAGAGATGATCTAACCTCCCTCAAGTCCCTGAGCA	900
DB	878	TCTCCCAACAGTCAAGATTAATCAGCAGAGATGATCTAACCTCCCTCAAGTCCCTGAGCA	937
QY	901	TCTACGTTTGT	960
DB	938	TCTACGTTTGT	997
QY	961	CACAACTTGGCTGCGGGAACACACAGAGATGATGATGATGATGATGATGATGATG	1020
DB	998	CACAACTTGGCTGCGGGAACACACAGAGATGATGATGATGATGATGATGATGATG	1057
QY	1021	ATGGGATGATGAGAGAGTGTCCAGACAGAGCTTAATCTGATGAGAGAGATTA	1080
DB	1058	ATGGGATGATGAGAGAGTGTTCAGACAGAGCTTAATCTGATGAGAGAGATTA	1117
QY	1081	GATTGTGATTAAGATTAATGAGCAACCTGAGTGGCTGATCACTTCAAGTGAATTTGA	1140
DB	1118	GATTGTGATTAAGATTAATGAGCAACCTGAGTGGCTGATCACTTCAAGTGAATTTGA	1177
QY	1141	CCGAGAACTCTTTTCAACAAATTCAGTACCAAAATGCTATGCTGCTGAATTTAA	1200
DB	1178	CCGAGAACTCTTTTCAACAAATTCAGTACCAAAATGCTATGCTGCTGAATTTAA	1237
QY	1201	CACCTCTATCAGTGGATCCCTCTGCTGAGACCTTTCAATTCATGACAGAAATA	1260
DB	1238	CACCTCTATCAGTGGATCCCTCTGCTGAGACCTTTCAATTCATGACAGAAATA	1297
QY	1261	CACTATCAACAGTTTATCTACAAACATCTATATGCTGAGCATGGAATTAACCACTT	1320
DB	1298	CACTATCAACAGTTTATCTACAAACATCTATATGCTGAGCATGGAATTAACCACTT	1357
QY	1321	TGTTGATCAATTCACAGGCAATTCCTGCGAGGTTGCTGCTGATGAGAAATGTTCCACC	1380
DB	1358	TGTTGATCAATTCACAGGCAATTCCTGCGAGGTTGCTGCTGATGAGAAATGTTCCACC	1417
QY	1381	CGCAGTACAGAAAGTATCAACAGGCTTCATTTGACAGAGAGAGATGAATACAGTGC	1440
DB	1418	CGCAGTACAGAAAGTATCAACAGGCTTCATTTGACAGAGAGAGATGAATACAGTGC	1477
QY	1441	TTTTAATGATGACCGCAACGCTTTATGCTGAAGCCCTGATGAATCATTTGAAGAACTTAC	1500
DB	1478	TTTTAATGATGACCGCAACGCTTTATGCTGAAGCCCTGATGAATCATTTGAAGAACTTAC	1537
QY	1501	AGAGAGAAAGAGATGCTGCAAGATTTGGAAGCATCTATGATGACATGATGCTGGA	1560
DB	1538	AGAGAGAAAGAGATGCTGCAAGATTTGGAAGCATCTATGATGACATGATGCTGGA	1597
QY	1561	GCTGTATCCTGACCTCTGCTGATGAAGAGCTCGGCGCAGATGCAATCTTTGCTGAACAT	1620
DB	1598	GCTGTATCCTGACCTCTGCTGATGAAGAGCTCGGCGCAGATGCAATCTTTGCTGAACAT	1657
QY	1621	GCTAAGATTGAGCAACATCTCTTGAAGAGATTAAGTATGATGATGATGATGATG	1680
DB	1658	GCTAAGATTGAGCAACATCTCTTGAAGAGATTAAGTATGATGATGATGATGATG	1717
QY	1681	TGCTAATGAG	1740
DB	1718	TGCTAATGAG	1777
QY	1741	CTCAATTCAGTCTCTCATCTGCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAG	1800
DB	1778	CTCAATTCAGTCTCTCATCTGCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAG	1837
QY	1801	TTCAGATCCAGAGCTTATTAACAGTCAACATCAATGCAAGTCTTCCGCTCCGAGCT	1860
DB	1838	TTCAGATCCAGAGCTTATTAACAGTCAACATCAATGCAAGTCTTCCGCTCCGAGCT	1897
QY	1861	AGATGATTAATCAATCCCAAGTACTACTAATAAGAGAGAGAGAGAGAGAGAGAG	1920
DB	1898	AGATGATTAATCAATCCCAAGTACTACTAATAAGAGAGAGAGAGAGAGAGAGAG	1957
QY	1921	TGATCATATTTATTTATTAATGAACCATGCTATTAATTAATTAATTAATTTT	1980



QY	241	ATTCTATGGAGAAA	CTGCTCAAC	CCGGATTTT	TGACAA	GATTAATTT	CTGAA	300
Db	278	ATTCTATGGAGAAA	CTGCTCAAC	CCGGATTTT	TGACAA	GATTAATTT	CTGAA	337
QY	301	ACCCACTCCAAA	CACAGTSCACT	CTACCTTAC	CCACTTCA	GGGATTTT	TGAAAGCTT	360
Db	338	ACCCACTCCAAA	CACAGTSCACT	CTACCTTAC	CCACTTCA	GGGATTTT	TGAAAGCTT	397
QY	351	GAAATACATTTCC	CTCTTTCG	AAATGCAATTA	TGAGTTAT	TGTGTG	ACATCCAGATCA	420
Db	398	GAAATACATTTCC	CTCTTTCG	AAATGCAATTA	TGAGTTAT	TGTGTG	ACATCCAGATCA	457
QY	421	TTTGATGACAGT	CCACCACTTA	CAATGCTAC	TATGCTTAC	CAAAAGCTGG	GAAGCTT	480
Db	458	TTTGATGACAGT	CCACCACTTA	CAATGCTAC	TATGCTTAC	CAAAAGCTGG	GAAGCTT	517
QY	481	CTTAACCTCTCT	TAATTA	CTAGAGCCCTT	CTCTGCTG	ATGATG	ATGATG	540
Db	518	CTTAACCTCTCT	TAATTA	CTAGAGCCCTT	CTCTGCTG	ATGATG	ATGATG	577
QY	541	CTTGAGTGTCAA	AGGTAA	AAAGACGCTT	CTGATTC	CAATGATG	ATGATG	600
Db	578	CTTGAGTGTCAA	AGGTAA	AAAGACGCTT	CTGATTC	CAATGATG	ATGATG	637
QY	601	TCTAAGAA	GAAGTTCA	TCCCTGAT	CCCCAGG	CTCAAA	CAATGATG	660
Db	638	TCTAAGAA	GAAGTTCA	TCCCTGAT	CCCCAGG	CTCAAA	CAATGATG	697
QY	661	CCAGCACTTCA	GCAGCACG	AGTTTTC	CAAGATCA	TAAGGAGG	GGCAGCTT	720
Db	698	CCAGCACTTCA	GCAGCACG	AGTTTTC	CAAGATCA	TAAGGAGG	GGCAGCTT	757
QY	721	CGGGCTGGG	CCATG	GGGCTGA	CTTAAT	TATTTA	CGGTGAA	780
Db	758	CGGGCTGGG	CCATG	GGGCTGA	CTTAAT	TATTTA	CGGTGAA	817
QY	781	TAAATCGG	CCCTTTT	CAAGATG	AAAAAT	TATCAG	TAAATTTA	840
Db	818	TAAATCGG	CCCTTTT	CAAGATG	AAAAAT	TATCAG	TAAATTTA	877
QY	841	TCCCTCCCA	AGTCAAA	GATACTC	AGAGATG	ATCA	CCCTCCTA	900
Db	878	TCCCTCCCA	AGTCAAA	GATACTC	AGAGATG	ATCA	CCCTCCTA	937
QY	901	TCTA	CGGTTG	CTG	TGGG	CAAGAG	GTCTTGA	960
Db	938	TCTA	CGGTTG	CTG	TGGG	CAAGAG	GTCTTGA	997
QY	961	CACAA	TCTGGCTG	GGGAA	CACAA	CAGATG	TGATG	1020
Db	998	CACAA	TCTGGCTG	GGGAA	CACAA	CAGATG	TGATG	1057
QY	1021	ATGGG	GTGATG	AGCAGT	TTTCC	AGACAG	AGCTTA	1080
Db	1058	ATGGG	GTGATG	AGCAGT	TTTCC	AGACAG	AGCTTA	1117
QY	1081	GATTG	ATTTGA	ATTTATG	CAACA	CTTGAG	TGCTTCA	1140
Db	1118	GATTG	ATTTGA	ATTTATG	CAACA	CTTGAG	TGCTTCA	1177
QY	1141	CCGAGA	ACTACTT	TTC	CAACAA	GAATTC	CGTAC	1200
Db	1178	CCGAGA	ACTACTT	TTC	CAACAA	GAATTC	CGTAC	1237
QY	1201	CACCTCT	ATCACTG	GCATCC	CTTCTG	CTGAC	ACCTTCA	1260
Db	1238	CACCTCT	ATCACTG	GCATCC	CTTCTG	CTGAC	ACCTTCA	1297
QY	1261	CAACTT	CAACAG	TTATCT	CAACAA	CTCTAT	ATTTG	1320
Db	1298	CAACTT	CAACAG	TTATCT	CAACAA	CTCTAT	ATTTG	1357
QY	1321	TGTTGA	TATCAT	TTC	CACAGG	CAAAAT	TGCTGG	1380
Db	1358	TGTTGA	TATCAT	TTC	CACAGG	CAAAAT	TGCTGG	1417
QY	1381	CGCAT	ACAGAA	AGTAT	CAACAG	CTTCC	ATTGAC	1440
Db	1418	CGCAT	ACAGAA	AGTAT	CAACAG	CTTCC	ATTGAC	1477
QY	1441	TTTTA	TGATG	ATCCG	CAAAAG	CTTTAT	AGCTTAT	1500
Db	1478	TTTTA	TGATG	ATCCG	CAAAAG	CTTTAT	AGCTTAT	1537
QY	1501	AGGAAA	AGTGA	AAATG	CTG	CAGATG	GAAGCA	1560
Db	1538	AGGAAA	AGTGA	AAATG	CTG	CAGATG	GAAGCA	1597
QY	1561	GCTG	ATCTG	CCCTT	CTG	TGAAA	AGCCCTG	1620
Db	1598	GCTG	ATCTG	CCCTT	CTG	TGAAA	AGCCCTG	1657
QY	1621	GGTAG	AGTTG	GAAG	CAACAT	TCTC	TGAAA	1680
Db	1658	GGTAG	AGTTG	GAAG	CAACAT	TCTC	TGAAA	1717
QY	1681	TGCTT	ACTG	GAAG	CAACAT	TCTC	TGAAA	1740
Db	1718	TGCTT	ACTG	GAAG	CAACAT	TCTC	TGAAA	1777
QY	1741	CTCA	ATTCAG	TCTCT	CAATCT	GC	CAATTA	1800
Db	1778	CTCA	ATTCAG	TCTCT	CAATCT	GC	CAATTA	1837
QY	1801	TCCAG	ATCCAG	AGCTCA	TAAAAC	AGTCA	CCATCA	1860
Db	1838	TCCAG	ATCCAG	AGCTCA	TAAAAC	AGTCA	CCATCA	1897
QY	1861	AGAT	GATAT	CAATCC	CACAT	CTA	CTA	1920
Db	1898	AGAT	GATAT	CAATCC	CACAT	CTA	CTA	1957
QY	1921	TGAT	CATAT	TTTAT	TTATTA	TATG	AAACAT	1980
Db	1958	TGAT	CATAT	TTTAT	TTATTA	TATG	AAACAT	2017
QY	1981	ATAT	TAAAC	CTTAT	CTTAT	CTTAT	CTTAT	2040
Db	2018	ATAT	TAAAC	CTTAT	CTTAT	CTTAT	CTTAT	2077
QY	2041	GAGAA	AGAGT	CACTAT	CTTGA	AGACTT	TATG	2100
Db	2078	GAGAA	AGAGT	CACTAT	CTTGA	AGACTT	TATG	2137
QY	2101	TGTTA	AGTTG	GA	AAACAG	TTTAT	TGTTAT	2160
Db	2138	TGTTA	AGTTG	GA	AAACAG	TTTAT	TGTTAT	2197
QY	2161	CGT	CTTTT	TA	CTGA	TTTCA	CTTAT	2220
Db	2198	CGT	CTTTT	TA	CTGA	TTTCA	CTTAT	2257
QY	2221	TAA	ACAT	ATCA	AGATG	CCAAAT	GCTG	2280
Db	2258	TAA	ACAT	ATCA	AGATG	CCAAAT	GCTG	2317
QY	2281	GAT	CTTCA	TATG	ATG	AAAGT	TTTAA	2340
Db	2318	GAT	CTTCA	TATG	ATG	AAAGT	TTTAA	2377
QY	2341	TTTTT	CTG	ATCA	CAAA	AAAGG	ATCA	2399
Db	2378	TTTTT	CTG	ATCA	CAAA	AAAGG	ATCA	2437
QY	2400	ACA	TTAC	AGTA	ATTTCA	TGCTACT	TTTAA	2459

Db	2438	ACATTCACAGTAATTTTCATGCTCTACTTTTAAATACGACATATAACATTAATTTGAAT	2497
QY	2460	TTCTCAATTCATAGGGTAGAATCACTGTAAAGCTTGTTGATTTCTTAAAGTTATTA	2519
Db	2498	TTCTCAATTCATAGGGTAGAATCACTGTAAAGCTTGTTGATTTCTTAAAGTTATTA	2557
QY	2520	ACTTGTACATATACCAAAAAGAGAGCTGCTGTGATTTAAATCTGTAAATCAATAGAAAT	2579
Db	2558	ACTTGTACATATACCAAAAAGAGAGCTGCTGTGATTTAAATCTGTAAATCAATAGAAAT	2617
QY	2580	TTTACTACCAATGGCTGTGTAAATATTTTATTAAGTATGTTCCCTTTTACCAAGATAT	2639
Db	2618	TTTACTACCAATGGCTGTGTAAATATTTTATTAAGTATGTTCCCTTTTACCAAGATAT	2677
QY	2640	AAACCTTTTATAGTGTGACTGTAAACCTTCCTTTTAAATCAAAATGCGAAATTTATTAAG	2699
Db	2678	AAACCTTTTATAGTGTGACTGTAAACCTTCCTTTTAAATCAAAATGCGAAATTTATTAAG	2737
QY	2700	GTGGTGAAGCCACCTGCAGCTGTATATCTCAAAATTAAGATATCCGTGTGAGATTTCCAGAA	2759
Db	2738	GTGGTGAAGCCACCTGCAGCTGTATATCTCAAAATTAAGATATTTGTGTAGATATTCAGAA	2797
QY	2760	TCTGTATATATAGCTGTGTATACATATTAATAAACCCCATACCCCGCCAAAGGGGTCTTACC	2819
Db	2798	TTTGTTTATATAGCTGTGTATACATATTAATAATCTATATACG-----AAAAGGTCTAAC	2850
QY	2820	CTTGAAACATTAAGCAATATACCAAAAGAGAAAAGCCAAATTTATGTTCCAAATTTAGGG	2879
Db	2851	TTTATA-----AATAGCAATTAACAAAGAGAAAAGCAAAATTTATGTTCCAAATTTAG	2901
QY	2880	TTTAAACCTTTTGAAGCAAACTTTTTTTTACCTTTGTGCACCTGTGAGACCTGTATCTAGA	2939
Db	2902	GTTTTAAACCTTTTGAAGCAAACTTTTTTTTACCTTTGTGCACCTGTGAGACCTGTATCTAGA	2961
QY	2940	TTTGTGATATAGGTTAATGAAGTACCAAGCTGTGCTTGAATTAACGATATGTTTTCTAGA	2999
Db	2962	TTTGTGATATAGGTTAATGAAGTACCAAGCTGTGCTTGAATTAACGATATGTTTTCTAGA	3021
QY	3000	TTTTCTGTGTACAGTTAATTTTATAGCACTGCATATCAATTCGAAAGTAGCAATGACCT	3059
Db	3022	TTTTCTGTGTGTACAGTTAATTTTATAGCACTGCATATCAATTCGAAAGTAGCAATGACCT	3081
QY	3060	CATATAAATACCTCTTCCAAAATGCTTAAATATCATTTCCACATTAATTTATCTAGACTT	3119
Db	3082	CATATAAATACCTCTTCCAAAATGCTTAAATATCATTTCCACATTAATTTATCTAGACTT	3141
QY	3120	GAAAGCAATTCAGTAGTGTGATGGAATCAAGCTGTGCTACCTGCATGCTGTCTCTTTTC	3179
Db	3142	GAAAGCAATTCAGTAGTGTGATGGAATCAAGCTGTGCTACCTGCATGCTGTCTCTTTTC	3201
QY	3180	TTTTCTTCTTTTATAGCAATTTTGTCTAAGAGACACAGCTCTTCTCAAAACCTTGCTTCTCT	3239
Db	3202	TTTTCTTCTTTTATAGCAATTTTGTCTAAGAGACACAGCTCTTCTCAAAACCTTGCTTCTCT	3260
QY	3240	ATTTGTGTTTACAGTTTAAAGATATAGAGTTCACTTTCTTTGAGACTCTGCTCTAATTTTC	3299
Db	3262	ATTTGTGTTTACAGTTTAAAGATATAGAGTTCACTTTCTTTGAGACTCTGCTCTAATTTTC	3320
QY	3300	TTACCTGAACCTTTTGCAGATTTTTCAGTAAACCTCAGCTCAGAGACTGCTATTTAGCTCT	3358
Db	3321	TTACCTGAACCTTTTGCAGATTTTTCAGTAAACCTCAGCTCAGAGACTGCTATTTAGCTCT	3380
QY	3360	CTTAAGAAGATTAATAAAAAAAAAAAAAA 3386	
Db	3381	CTTAAGAAGATTAATAAAAAAAAAAAAAA 3407	

Query Match	Best Local Similarity	Score	DB	Length	Matches
97.7%	Pred. No. 0;	3216.6;	DB 16;	Length 4465;	
0;	Mismatches	59;	Indels	18;	Gaps
3310;	Conservative	0;			
1	GTCCAGGAACCTCCACGAGCGCCTCTTCAGCTTCACAGCCAGACGCGCTTCAGACGCA	60			
38	GTCCAGGAACCTCCACGAGCGCCTCTTCAGCTTCACAGCCAGACGCGCTTCAGACGCA	97			
61	AAAGCTTACCCCGGCGCGCGCCCTGCGCGCTTCAGTGTGCGCGCGCGCGCTTCAGTGT	120			
98	AAAGCTTACCCCGGCGCGCGCGCCCTGCGCGCTTCAGTGTGCGCGCGCGCGCTTCAGTGT	157			
121	GTGCGCGGCTCCGCGCGCTTCAGCCATACAGCAATCTCTGCTTCCACCCATGTCAAA	180			
158	GTGCGCGGCTCCGCGCGCTTCAGCCATACAGCAATCTCTGCTTCCACCCATGTCAAA	217			
181	CCGAGGTGTATGTATGAGTGTGGATTTGACAGCATATAGTGCATTTGATCCCGGACAGG	240			
218	CCGAGGTGTATGTATGAGTGTGGATTTGACAGCATATAGTGCATTTGATCCCGGACAGG	277			
241	ATTCTATGAGAAAGCTGTCTCAACACCGGAATTTTGTGCAAGAAATTAATTTCTGAA	300			
278	ATTCTATGAGAAAGCTGTCTCAACACCGGAATTTTGTGCAAGAAATTAATTTCTGAA	337			
301	ACCGACTCCAAACACAGTGCATCATATTTACCATTTCAAGGATTTTGGACGTTGT	360			
338	ACCGACTCCAAACACAGTGCATCATATTTACCATTTCAAGGATTTTGGACGTTGT	397			
361	GATTAACATTCCTCTTCGAAATGCAATTAATGATTAATGTTGACATCCAGATCACA	420			

D	b	398	GAATTAACATTCCTCTCTCGAATATGCAATTAAGTTATGTTCTTGACATCCAGATCA	457
Q	y	421	TTTATTTGACAGATCCACCAACTTACANATGAGTATAGGCTACAAAAGCTGGAGACCTT	480
D	b	458	TTTATTTGACAGATCCACCAACTTACANATGAGTATAGGCTACAAAAGCTGGAGACCTT	517
Q	y	481	CTTAACTCTCTCTATTAATATAGAGCCCTTCTCTGTCCTGATGATTTGCCCGACCTC	540
D	b	518	CTCAACCTCTCTATTAATATAGAGCCCTTCTCTGTCCTGATGATTTGCCCGACCTC	577
Q	y	541	CTTGGGTTGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG	600
D	b	578	CTTGGGTTGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG	637
Q	y	601	TCTAAGAGAAAGTATATCCCTGATCCCAAGGCTCAACATGATGTTGGCATTTCTTGC	660
D	b	638	TCTAAGAGAAAGTATATCCCTGATCCCAAGGCTCAACATGATGTTGGCATTTCTTGC	697
Q	y	661	CCAGCATTTGACGACCCAGTTTTCAGACAGATCATTAAGCAGGCGCAGCTTTCACCA	720
D	b	698	CCAGCATTTGACGACCCAGTTTTCAGACAGATCATTAAGCAGGCGCAGCTTTCACCA	757
Q	y	721	CGGGCTGGGCGATGGGCTGATCTTAATCATTTACGTTGAACTCTGGCTTACAGCG	780
D	b	758	CGGGCTGGGCGATGGGCTGATCTTAATCATTTACGTTGAACTCTGGCTTACAGCG	817
Q	y	781	TAAACTGCGCTTTTCAAGATGAGAAATGAAATATCAGATTAATTGATGAGAAATGTA	840
D	b	818	TAAACTGCGCTTTTCAAGATGAGAAATGAAATATCAGATTAATTGATGAGAAATGTA	877
Q	y	841	TCTCTCCACAGTCAAAAGATATCTCAGCAGAGATGATCTACCTCTCAAGTCCCTGAGA	900
D	b	878	TCTCTCCACAGTCAAAAGATATCTCAGCAGAGATGATCTACCTCTCAAGTCCCTGAGA	937
Q	y	901	TCTAAGGTTTGTCTGTGGGCAAGAGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
D	b	938	TCTAAGGTTTGTCTGTGGGCAAGAGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT	997
Q	y	961	CACAACTCTGCTGGGGAACACACAGAGATGATGATGCTTAAACAGAGATCCCTGA	1020
D	b	998	CACAACTCTGCTGGGGAACACACAGAGATGATGATGCTTAAACAGAGATCCCTGA	1057
Q	y	1021	ATGGGGTGTATGAGCAGTTGTTCCAGACAGCAGGCTTAATCTGATGAGAGACTATTA	1080
D	b	1058	ATGGGGTGTATGAGCAGTTGTTCCAGACAGCAGGCTTAATCTGATGAGAGACTATTA	1117
Q	y	1081	GATTTGATGTAAGTATATATGTCACACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1140
D	b	1118	GATTTGATGTAAGTATATATGTCACACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1177
Q	y	1141	CCAGAACTACTTTTCAACAAACATTCAGATCCAAATGATGTTGTGTGTGTGTGTGT	1200
D	b	1178	CCAGAACTACTTTTCAACAAACATTCAGATCCAAATGATGTTGTGTGTGTGTGTGT	1237
Q	y	1201	CACCTCTATATCATGTCATCCCTTCTGCTGACACTTTCAAAATTCATGACCAAGATA	1260
D	b	1238	CACCTCTATATCATGTCATCCCTTCTGCTGACACTTTCAAAATTCATGACCAAGATA	1297
Q	y	1261	CACCTCTATATCATGTCATCCCTTCTGCTGACACTTTCAAAATTCATGACCAAGATA	1320
D	b	1298	CACCTCTATATCATGTCATCCCTTCTGCTGACACTTTCAAAATTCATGACCAAGATA	1357
Q	y	1321	TGTTGAATCATTCACAGCAAAATTTGCTGCGAGGTTGCTGTGTGTGTGTGTGTGTGT	1380
D	b	1358	TGTTGAATCATTCACAGCAAAATTTGCTGCGAGGTTGCTGTGTGTGTGTGTGTGTGT	1417
Q	y	1381	CGCAGTACAGAAAGTATATCAGGCTCTCATTTGACACAGCAGGAGATGAAATACAGTC	1440
D	b	1418	CGCAGTACAGAAAGTATATCAGGCTCTCATTTGACACAGCAGGAGATGAAATACAGTC	1477
Q	y	1441	TTTTATATAGTACCGCAAAAGCTTTATGCTGAACCTTATGAAATCATTTTGAAGACTTAC	1500
D	b	1478	TTTTATATAGTACCGCAAAAGCTTTATGCTGAACCTTATGAAATCATTTTGAAGACTTAC	1537
Q	y	1501	AGAGAAAAAGAAATGTTCTGAGAGTTGAGACACTGATATGATGACATGATGCTGTGA	1560
D	b	1538	AGAGAAAAAGAAATGTTCTGAGAGTTGAGACACTGATATGATGACATGATGCTGTGA	1597
Q	y	1561	GCTGATTCCTGCTCTGCTGTGTAAGAAAGCTCGGCGAGATGCATCTTTGGTGAACAT	1620
D	b	1598	GCTGATTCCTGCTCTGCTGTGTAAGAAAGCTCGGCGAGATGCATCTTTGGTGAACAT	1657
Q	y	1621	GCTGATTCCTGCTCTGCTGTGTAAGAAAGCTCGGCGAGATGCATCTTTGGTGAACAT	1680
D	b	1658	GCTGATTCCTGCTCTGCTGTGTAAGAAAGCTCGGCGAGATGCATCTTTGGTGAACAT	1717
Q	y	1681	TGCTTACTGTAAGCAAGCACTTTTGGTGTGAGAGAGTGGTTTCAATCATCAACTGC	1740
D	b	1718	TGCTTACTGTAAGCAAGCACTTTTGGTGTGAGAGAGTGGTTTCAATCATCAACTGC	1777
Q	y	1741	CTCAATTCAGTCTCTCATCTGCAATTAACGTAAGGCTGTCCCTTTACCTTCAATCAGT	1800
D	b	1778	CTCAATTCAGTCTCTCATCTGCAATTAACGTAAGGCTGTCCCTTTACCTTCAATCAGT	1837
Q	y	1801	TCCAGATCCAGAGCTCATTTAAACAGTCAACATCATGAAATGTAAGTCTCCGCTCCGACT	1860
D	b	1838	TCCAGATCCAGAGCTCATTTAAACAGTCAACATCATGAAATGTAAGTCTCCGCTCCGACT	1897
Q	y	1861	AGATGATATCAATCCACAGTACTACTTAAAGAGAGGCTGACATGAACTGTGAGAGCTTAA	1920
D	b	1898	AGATGATATCAATCCACAGTACTACTTAAAGAGAGGCTGACATGAACTGTGAGAGCTTAA	1957
Q	y	1921	TGATCATATTTATTTATTTATTAAGAACATGCTATTTATTTATTTATTTATTTATTTAT	1980
D	b	1958	TGATCATATTTATTTATTTATTTATTAAGAACATGCTATTTATTTATTTATTTATTTAT	2017
Q	y	1981	ATATTTAACTCTTATGTTACTTAAACATCTTCTGTAACAGAGTCAAGTCTCTGTTGG	2040
D	b	2018	ATATTTAACTCTTATGTTACTTAAACATCTTCTGTAACAGAGTCAAGTCTCTGTTGG	2077
Q	y	2041	GAGAAAGAGTCAATCTTGTGAAGCTTTATATGCTCACTCACTTAAAGATTTGCTGTGC	2100
D	b	2078	GAGAAAGAGTCAATCTTGTGAAGCTTTATATGCTCACTCACTTAAAGATTTGCTGTGC	2137
Q	y	2101	TGTTAGTTTGGAAAACAGTTTATTTCTGTTTATTAACACAGAGAAATGATGTTTGA	2160
D	b	2138	TGTTAGTTTGGAAAACAGTTTATTTCTGTTTATTAACACAGAGAAATGATGTTTGA	2197
Q	y	2161	CGTCTTTTACTTGAATTTCACTATATTTATTAAGAGCAAGATGATGTTTGAATG	2220
D	b	2198	CGTCTTT	

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QY 2580 TTTACTACAAATGCTGTTAAATATTTTAAATGATAGTCTCTTTTCAACCAAGATAT 2639
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Db 3381 CTTAAGAGATTAATAAAAAAAAAAAAAA 3407

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RESULT 8
US-10-373-801-11
; Sequence 11, Application US/10373801
; Publication No. US20040005644A1
; GENERAL INFORMATION:
; APPLICANT: Yibai Pharmaceutical (USA)
; TITLE OF INVENTION: Method and composition for detection and treatment of breast cano
; FILE REFERENCE: 12399.00
; CURRENT APPLICATION NUMBER: US/10/373,801
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 4465
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-373-801-11
Query Match 95.0%; Score 3216.6; DB 16; Length 4465;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 3310; Conservative 0; Mismatches 59; Indels 18; Gaps 4;
QY 1 GTCCAGGATCTCTCAGCAGAGCTCTCTTCAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCA 60
Db 38 GTCCAGGATCTCTCAGCAGAGCTCTCTTCAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCA 97
QY 61 AAGCTTACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
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QY 121 GTGGCGGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
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Db 398 GAATTAATTCCTCTCTCTTCAAAATGCAATTAATGATATGTTGACATCAATCA 457
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QY 481 CTCTAACCTCTCTATTAATTAATGAGCCCTCTCTCTGCTGCTGATGATGATGATGATG 540
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QY 541 CTGGGTGTCAAGAGTAAAGACAGCTTCTGATTAATGATGATGATGATGATGATGATG 600
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Db 638 TCTAAGAAAGATTCATCCCTGATCCCGAGGCTCAAAATGATGATGATGATGATGATG 697
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Db 698 CCAGACTTCAGCAGCAGATTTTCAAGACAGATCAATAGCAGAGGCGCAGCTTCAACAA 757
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Qy 1261 CAACATACAGATTAATCTACACAACTCTATATTTGCTGGAACATGGAATTTACCAATT 1320  
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Qy 1921 TGATCATATTTATTTATTAATGAACCATGTCTATTAATTTATTTAATTAATATTT 1980  
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QY 1561 GCGTATCGTCCCTTCTGTAGAAAAGCCTCGGCCAGATGCCATCTTTGTGAACCAT 1620  
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Db 3351 CTTAAGAAATTTAAAAAAGAAAAA 3377

RESULT 10  
US-10-071-766-46  
; Sequence 46, Application US/10071766  
; Publication No. US20020192678A1  
; GENERAL INFORMATION:  
; APPLICANT: Huel-Mei Chen  
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE  
; FILE REFERENCE: PA-0043 US  
; CURRENT APPLICATION NUMBER: US/10/071,766  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 144  
; SOFTWARE: PERL Program  
; SEQ ID NO 46  
; LENGTH: 4496  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020192678A1 271804.3  
US-10-071-766-46

Query Match 94.9%; Score 3215; DB 14; Length 4496;  
Best Local Similarity 97.7%; Pred. No. 0;  
Matches 3309; Conservative 0; Mismatches 60; Indels 18; Gaps 4;

1 GTCCAGAACCTCCAGAGAGGCTCCCTTCAGCTCCACAGCCAGAGCCCTCAGACAGCA 60  
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61 AAGCCTAACCCCGCGCGCGCCCTGCGCGCGCTGCGAGTCTGCGCGCGCTGCT 120  
68 AAGCCTAACCCCGCGCGCGCCCTGCGCGCGCTGCGAGTCTGCGCGCGCTGCT 127  
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 ; GENERAL INFORMATION:  
 ; APPLICANT: Mikita, Thomas  
 ; APPLICANT: Shiffman, Dov  
 ; APPLICANT: Porter, Gordon, J.  
 ; APPLICANT: Kaser, Matthew R.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
 ; FILE REFERENCE: PA-0050 US  
 ; CURRENT APPLICATION NUMBER: US/10/247, 671  
 ; PRIOR FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: 60/323,784  
 ; PRIOR FILING DATE: 2001-09-19  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 126  
 ; LENGTH: 4750  
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 ; ORGANISM: Homo sapiens  
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; LOCATION: 2551
; OTHER INFORMATION: a, t, c, g, or other
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Query Match 74.2%; Score 2513.4; DB 14; Length 2563;
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QY 181 CCGAGGTGTATGTATGAGTGTGGATTTGACCAAGTATAGTGCATTTGCCAGCAGG 240
Db 188 CCGAGGTGTATGTATGAGTGTGGATTTGACCAAGTATAGTGCATTTGCCAGCAGG 247
QY 241 ATTCTATGAGAAACGTCAACACCGGAATTTTACAGAAATTAATTTTCTGAA 300
Db 248 ATTCTATGAGAAACGTCTACACCGGAATTTTACAGAAATTAATTTTCTGAA 307
QY 301 ACCGACTCAAAACAGTGCATACATACCTTCAAGGAAATTTTGAAGCTTGT 360
Db 308 ACCGACTCAAAACAGTGCATACATACCTTCAAGGAAATTTTGAAGCTTGT 367
QY 361 GAATTAATTCCTCTCTTGAATGCAATTTATAGTTATGTGTGATCATCAATCA 420
Db 368 GAATTAATTCCTCTCTTGAATGCAATTTATAGTTATGTGTGATCATCAATCA 427
QY 421 TTGATGAGAGTCCACCACTTACATGCTAGTATAGCTAGCAAAAGCTGGGAAGCTT 480
Db 428 TTGATGAGAGTCCACCACTTACATGCTAGTATAGCTAGCAAAAGCTGGGAAGCTT 487
QY 481 CTCTAACCTCTCTATTATATAGAGCTTCTCTGTGCTGATGATGCTCCGACTCC 540
Db 488 CTCTAACCTCTCTATTATATAGAGCTTCTCTGTGCTGATGATGCTCCGACTCC 547
QY 541 CTGGGTGTCAAGGTAAAGAGAGCTTCTGATTAATGAGATTTGAAAAATTTGCT 600
Db 548 CTGGGTGTCAAGGTAAAGAGAGCTTCTGATTAATGAGATTTGAAAAATTTGCT 607
QY 601 TCTAAGAGAAAGTTCAATCCCTGATCCCGAGGCTCAAAATGATGTTGATCTTTC 660
Db 608 TCTAAGAGAAAGTTCAATCCCTGATCCCGAGGCTCAAAATGATGTTGATCTTTC 667
QY 661 CAGACACTTCAGCAGCAGGTTTTCAGAGATCATTAACGAGGCGCAGCTTTCACCA 720
Db 668 CAGACACTTCAGCAGCAGGTTTTCAGAGATCATTAACGAGGCGCAGCTTTCACCA 727
QY 721 CGGGCTGGGCGATGGGTGAGCTTAATCATATTACGTGAAACTCTGTGACAGCG 780
Db 728 CGGGCTGGGCGATGGGTGAGCTTAATCATATTTCGTGAAACTCTGTGACAGCG 787
QY 781 TAAACTGCGGCTTTTCAAGGATGAAATGAATTCAGATTAATGATGATGAGATGTA 840
Db 788 TAAACTGCGGCTTTTCAAGGATGAAATGAATTCAGATTAATGATGATGAGATGTA 847
QY 841 TCTCTCCACAGTCAAGATATCAGCAGAGATGATCTCTCTCAAGTCTCTGAGCA 900
Db 848 TCTCTCCACAGTCAAGATATCAGCAGAGATGATCTCTCTCAAGTCTCTGAGCA 907
QY 901 TCTAGGTTTGTGTGGGAGAGAGTCTTTGTCTGTGTCTGTGTGTATGTATGC 960
Db 908 TCTAGGTTTGTGTGGGAGAGAGTCTTTGTGTGTGTCTGTGTGTATGTATGC 967

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RESULT 12
US-10-044-090-477
; Sequence 477, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 477
; LENGTH: 2563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20020137081A1 1217831CBI

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US-09-954-456-324

Query Match 51.0%; Score 1727; DB 9; Length 9453;  
 Best Local Similarity 96.1%; Pred. No. 0;  
 Matches 1818; Conservative 0; Mismatches 55; Indels 18; Gaps 4;

QY 1497 TTACAGAGAGAGAGAGAGATGTCTGACAGAGTGGAGACCTCTATGGTGCATCGATGCTG 1556  
 DB TCACAGAGAGAGAGAGAGATGTCTGACAGAGTGGAGACCTCTATGGTGCATCGATGCTG 6547  
 QY 1557 TGGAGACTGTATCTCCCTCTCTGTGAGAGAAACCTCCGCGACATGCCATCTTTGGTAAA 1616  
 DB TGGAGACTGTATCTCCCTCTCTGTGAGAGAAACCTCCGCGACATGCCATCTTTGGTAAA 6607  
 QY 1617 CCATGGTGAAGTGTGAGACCACTTCTCTGAGAGAGCTTATGGGTATGTTATATGTT 1676  
 DB CCATGGTGAAGTGTGAGACCACTTCTCTGAGAGAGCTTATGGGTATGTTATATGTT 6667  
 QY 1677 CTCCTGCTTACTGAGAGCCAGCACTTTGTGAGAGAGTGGGTTTTCAMATCATCAACA 1736  
 DB CTCCTGCTTACTGAGAGCCAGCACTTTGTGAGAGAGTGGGTTTTCAMATCATCAACA 6727  
 QY 1737 CTGCTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTTACTTTATCA 1796  
 DB CTGCTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGTCCCTTTACTTTATCA 6787  
 QY 1797 GTGTTCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTCTTCCGCTCG 1856  
 DB GTGTTCAGATCCAGAGCTCATTTAAACAGTCAACATCAATGCAAGTCTTCCGCTCG 6847  
 QY 1857 GACTGATGATATCAATCCACAGTACTTAAAGAAAGTTCGACTGAAGTGAAGT 1916  
 DB GACTGATGATATCAATCCACAGTACTTAAAGAAAGTTCGACTGAAGTGAAGT 6907  
 QY 1917 CTAAGATCATATTTATTTATTTATGAAACATCTCTATTAATTTATTTATTAAT 1976  
 DB CTAAGATCATATTTATTTATTTATGAAACATCTCTATTAATTTATTTATTAAT 6967  
 QY 1977 ATTATATTTAAACCTCTTATGTACTTAAACATCTCTGTAACAGAGTCAAGTCCGT 2036  
 DB ATTATATTTAAACCTCTTATGTACTTAAACATCTCTGTAACAGAGTCAAGTCCGT 7027  
 QY 2037 TGGGAGAGAGAGTCAATCTGTGAGAGCTTTTATGTCACTACTTAAAGATTTTGTG 2096  
 DB TGGGAGAGAGAGTCAATCTGTGAGAGCTTTTATGTCACTACTTAAAGATTTTGTG 7087  
 QY 2097 TTGCTGTATAGTTGGAGAGAGCTTTTATCTGTTTATTAACAGAGAGAAATGAGTT 2156  
 DB TTGCTGTATAGTTGGAGAGAGCTTTTATCTGTTTATTAACAGAGAGAAATGAGTT 7147  
 QY 2157 TTGAGCTCTTTTACTGTGAATTTCACTTATTTAAAGAGAGAAATGAGTTGA 2216  
 DB TTGAGCTCTTTTACTGTGAATTTCACTTATTTAAAGAGAGAAATGAGTTGA 7207  
 QY 2217 ATACTTAAACACTATCAAGATGCAAAATGCTGAAAGTTTTCACGCTGATGTTTC 2276  
 DB ATACTTAAACACTATCAAGATGCAAAATGCTGAAAGTTTTCACGCTGATGTTTC 7267  
 QY 2277 CAATGCACTCTCCAGATGATGATTAAGAGTAACTATGTTGAATTTTAAAGTACTTTG 2336  
 DB CAATGCACTCTCCAGATGATGATTAAGAGTAACTATGTTGAATTTTAAAGTACTTTG 7327  
 QY 2337 GGTATTTTCTGTCAATCAAC-AAAAAGGATCTAGTGAATTAATGAATTTTAA 2395  
 DB GGTATTTTCTGTCAATCAACAAAAAGGATCTAGTGAATTAATGAATTTTAA 7387  
 QY 2396 TTAGACATTAACAGTAATTTCACTTTTAAATCAGCAATGAAGAAATATTTG 2455  
 DB TTAGACATTAACAGTAATTTCACTTTTAAATCAGCAATGAAGAAATATTTG 7447  
 QY 2456 AAATTTCTAAATTCATAGGTTGAGATCACTGTAAAGCTTGTGATTTCTTAAAGTTA 2515  
 DB AAATTTCTAAATTCATAGGTTGAGATCACTGTAAAGCTTGTGATTTCTTAAAGTTA 7507

QY 2516 TTAAACTGTATATATCAAAAGAGAGCTGTCTGATTTAAATCTGTAAATCAGATG 2575  
 DB TTAAACTGTATATATCAAAAGAGAGCTGTCTGATTTAAATCTGTAAATCAGATG 7508  
 QY 2576 AAATTTTACTCAATTTGCTTTTAAATATTTTATTAAGTATGTTCTTTTTCACCAAGA 2635  
 DB AAATTTTACTCAATTTGCTTTTAAATATTTTATTAAGTATGTTCTTTTTCACCAAGA 7568  
 QY 2636 GTATTAACCTTTTAAAGTGTGATGATTAACCTTCTTTTAAATGCAAAATTTAT 2695  
 DB GTATTAACCTTTTAAAGTGTGATGATTAACCTTCTTTTAAATGCAAAATTTAT 7628  
 QY 2696 TAAAGTGTGAGAGCCAGTGTATCTCAAAATTAAGAAATCTGTTGAGATTTCC 2755  
 DB TAAAGTGTGAGAGCCAGTGTATCTCAAAATTAAGAAATCTGTTGAGATTTCC 7688  
 QY 2756 AGAATCTGTATATGCTGTGATCAATGTAAGAGAGAGAGAGAGAGAGAGAGAG 2815  
 DB AGAATCTGTATATGCTGTGATCAATGTAAGAGAGAGAGAGAGAGAGAGAGAG 7748  
 QY 2816 TACCTTGAACATTAAGAGATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2875  
 DB TACCTTGAACATTAAGAGATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 7801  
 QY 2876 AGAGTTTAACTTTTGAAGCACTTTTGTAGCTGTGAGAGAGAGAGAGAGAGAG 2935  
 DB AGAGTTTAACTTTTGAAGCACTTTTGTAGCTGTGAGAGAGAGAGAGAGAGAG 7852  
 QY 2936 CAGATTTTGTATAGAGTTAATGAAGTCAAGCTGTGATTAAGAGAGAGAGAGAG 2995  
 DB CAGATTTTGTATAGAGTTAATGAAGTCAAGCTGTGATTAAGAGAGAGAGAGAG 7912  
 QY 2996 CAGATTTTGTATAGAGTTAATGAAGTCAAGCTGTGATTAAGAGAGAGAGAGAG 3055  
 DB CAGATTTTGTATAGAGTTAATGAAGTCAAGCTGTGATTAAGAGAGAGAGAGAG 7972  
 QY 3056 ACCTCATTAATACCTCTTCAAAATGCTTAAATTCATTTCAACATTTATTTATCTGAG 3115  
 DB ACCTCATTAATACCTCTTCAAAATGCTTAAATTCATTTCAACATTTATTTATCTGAG 8032  
 QY 3116 TCTTGAAGCCAAATTCAGTATGAGTGAATGAAGTCAAGCTGTGATTAAGAGAGAG 3175  
 DB TCTTGAAGCCAAATTCAGTATGAGTGAATGAAGTCAAGCTGTGATTAAGAGAGAG 8092  
 QY 3176 TTTCTTTTCTTTTACCAATTTTGTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 3235  
 DB TTTCTTTTCTTTTACCAATTTTGTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 8152  
 QY 3236 TCCATTTTGTATTTTACTGATTTTAAAGATCAAGTTCATTTCTTTGAGAGTCTGCTATAT 3295  
 DB TCCATTTTGTATTTTACTGATTTTAAAGATCAAGTTCATTTCTTTGAGAGTCTGCTATAT 8211  
 QY 3296 TTTCTTACCTGAACCTTTTGAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 3355  
 DB TTTCTTACCTGAACCTTTTGAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 8271  
 QY 3356 TCCCTTTTAAAGATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3386  
 DB TCCCTTTTAAAGATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8331

RESULT 14  
 US-09-949-293-25  
 ; Sequence 25, Application US/09949293  
 ; Publication No. US2003008250A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thomann, Hans-Ulrich  
 ; APPLICANT: Wall, Kristian  
 ; APPLICANT: Fitzgerald, Michael  
 ; TITLE OF INVENTION: MUTATIONS OF THE CYCLOOXYGENASE-2 GENE  
 ; FILE REFERENCE: TECH01-07  
 ; CURRENT APPLICATION NUMBER: US/09/949, 293



; CURRENT FILING DATE: 2002-06-04  
 ; PRIOR APPLICATION NUMBER: 60/231,250  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 25  
 ; LENGTH: 11064  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-949-293-25

Query Match 50.7%; Score 1717.4; DB 10; Length 11064;  
 Best Local Similarity 95.8%; Pred. No. 0;  
 Matches 1812; Conservative 0; Mismatches 61; Indels 18; Gaps 4;

QY	1497	TTACAGGAGAAAGAAATGTCGAGAGTGTGAAAGCACTCTATGTGACATCATGCTG	1556
DB	7899	TCACAGGAGAAAGAAATGTCGAGAGTGTGAAAGCACTCTATGTGACATCATGCTG	7958
QY	1557	TGAGAGCTGATCCCTGCTTCTGTAGAAAGCTCGGCGAGATGCGCATCTTGGTGAAA	1616
DB	7959	TGAGAGCTGATCCCTGCTTCTGTAGAAAGCTCGGCGAGATGCGCATCTTGGTGAAA	8018
QY	1617	CCATGCTAGAAATGAGAGCACTTCTCTTGAAGAGCTTATGGGTAATGTTATATGTT	1676
DB	8019	CCATGCTAGAAATGAGAGCACTTCTCTTGAAGAGCTTATGGGTAATGTTATATGTT	8078
QY	1677	CTCCGCTACTGAGAGGCAACGACCTTTGTGAGAGAGTGGTTTCAAAATCATCAACA	1736
DB	8079	CTCCGCTACTGAGAGGCAACGACCTTTGTGAGAGAGTGGTTTCAAAATCATCAACA	8138
QY	1737	CTGCTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCCCTTACTTCAATCA	1796
DB	8139	CTGCTCAATTCAGTCTCTCATCTGCAATTAAGTGAAGGCTGCTCCCTTACTTCAATCA	8198
QY	1797	GTTGTCAGATCCAGAGCTCATTTAAACAATCAATCAATCAATGTTCTCCGCTCG	1856
DB	8199	GTTGTCAGATCCAGAGCTCATTTAAACAATCAATCAATCAATGTTCTCCGCTCG	8258
QY	1857	GACTGATGATATCAATCCACAGATCACTTAAGAAAGCGTGCAGCTGATGAACT	1916
DB	8259	GACTGATGATATCAATCCACAGATCACTTAAGAAAGCGTGCAGCTGATGAACT	8318
QY	1917	CTAATGATCATATTTATTTATTTATATGACCAAGCTATTAATTAATTAATTAAT	1976
DB	8319	CTAATGATCATATTTATTTATTTATATGACCAAGCTATTAATTAATTAATTAAT	8378
QY	1977	ATTATATTTAAATCTCTTATGTTACTTAAATCTTCTGTAACAGAGTCACTCTCTGT	2036
DB	8379	ATTATATTTAAATCTCTTATGTTACTTAAATCTTCTGTAACAGAGTCACTCTCTGT	8438
QY	2037	TGCGAGAGAAAGGAGCATCTGTAAGAGCTTTATGTCACACTCTAAAGTTTTGCTG	2096
DB	8439	TGCGAGAGAAAGGAGCATCTGTAAGAGCTTTATGTCACACTCTAAAGTTTTGCTG	8498
QY	2097	TTGCTGTTAAGTTTGAAGAAAGCTTTTATCTGTTTAAACAGAGAAATGAGTT	2156
DB	8499	TTGCTGTTAAGTTTGAAGAAAGCTTTTATCTGTTTAAACAGAGAAATGAGTT	8558
QY	2157	TTGAGAGCTTTTACTTGAATTTCACTTAATTTAAAGAGCAAGTAAGATGTTTGA	2216
DB	8559	TTGAGAGCTTTTACTTGAATTTCACTTAATTTAAAGAGCAAGTAAGATGTTTGA	8618
QY	2217	ATACTTAACAACATATCACAAGATGCAAAATGCTAAAGTTTTCACATGTCGATGTTT	2276
DB	8619	ATACTTAACAACATATCACAAGATGCAAAATGCTAAAGTTTTCACATGTCGATGTTT	8678
QY	2277	CAATGATCTTCCATGATGATTAAGAGTAATCTAATGTTTGAATTTTAAAGTACTTTG	2336
DB	8679	CAATGATCTTCCATGATGATTAAGAGTAATCTAATGTTTGAATTTTAAAGTACTTTG	8738
QY	2337	GGTATTTTCTGTCTCAAC-AAAAAGGTATCGTCGATTTAAATGAATATTTAA	2395

DB	8739	GTTATTTTCTGTCTATCAAAACAAAAAGGATCAGTCGATTTAATGAATTTTAA	8798
QY	2396	TTAGACATTTACAGTAATTTCAATGCTACTTTTAAATCAGCAATGAACATATTTG	2455
DB	8799	TTAGACATTTACAGTAATTTCAATGCTACTTTTAAATCAGCAATGAACATATTTG	8858
QY	2456	AAATTTCAAAATTCAGAGGATGAAATCACCTGTAAGAGCTGTTGATTTCTTAAAGTTA	2515
DB	8859	AAATTTCAAAATTCAGAGGATGAAATCACCTGTAAGAGCTGTTGATTTCTTAAAGTTA	8918
QY	2516	TTAAACTGTATACATATACCAAAAGAGCTGCTTGAATTAATCTGTAATTAATGAGATG	2575
DB	8919	TTAAACTGTATACATATACCAAAAGAGCTGCTTGAATTAATCTGTAATTAATGAGATG	8978
QY	2576	AAATTTACTACAAATTCGTTGTAATTAATTTTAAGTGAATGTTCTTTTACCAAGA	2635
DB	8979	AAATTTACTACAAATTCGTTGTAATTAATTTTAAGTGAATGTTCTTTTACCAAGA	9038
QY	2636	GTAATAACCTTTTGTGAGCTGTTAAACCTTCTTTTAAATCAAAATGCAAAATTTAT	2695
DB	9039	GTAATAACCTTTTGTGAGCTGTTAAACCTTCTTTTAAATCAAAATGCAAAATTTAT	9098
QY	2696	TAAAGTGTGAGAGCCATGCACTGATCTCAAAATTAAGATATCTGTTGATATTC	2755
DB	9099	TAAAGTGTGAGAGCCATGCACTGATCTCAAAATTAAGATATCTGTTGATATTC	9158
QY	2756	AGATCTGTTATATGCTGTGTAACATGTAATAAACCCTATACCCCGCAAAAGGGTCC	2815
DB	9159	AGATCTGTTATATGCTGTGTAACATGTAATAAATCTATATGCG-----AAAAGGGTCC	9211
QY	2816	TACCTTGAACATTAAGCAATTAACCAAGAGAGAAAGCCCAATATTGTTCCAAATTT	2875
DB	9212	TACCTTTAA-----AATTAAGCAATTAACCAAGAGAGAAAGCCCAATATTGTTCCAAAT	9262
QY	2876	AGGTTTAACTTTTGAAGCAACTTTTGTGAGCTGAGAGCTGATCT	2935
DB	9263	TTAGGTTTAACTTTTGAAGCAACTTTTGTGAGCTGAGAGCTGATCT	9322
QY	2936	CAGATTTGCTATAGAGTTAATGAAGTACCAAGCTGCTGTAATAAGATATGTTTCT	2995
DB	9323	CAGATTTGCTATAGAGTTAATGAAGTACCAAGCTGCTGTAATAAGATATGTTTCT	9382
QY	2996	CAGATTTCTGTGACAGTTTAAATTTAGCAGTCCATATCACTGCAAAAGTACATG	3055
DB	9383	CAGATTTCTGTGACAGTTTAAATTTAGCAGTCCATATCACTGCAAAAGTACATG	9442
QY	3056	ACCTCATTAATTAACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTATCTGAG	3115
DB	9443	ACCTCATTAATTAACCTCTTCAAAATGCTTAATTCATTTCAACATTAATTTATCTGAG	9502
QY	3116	TCTTGAAGCAATTCAGTAAGGATGATGGAATCAAGCTGCTGATCTGATGCTGCTT	3175
DB	9503	TCTTGAAGCAATTCAGTAAGGATGATGGAATCAAGCTGCTGATCTGATGCTGCTT	9562
QY	3176	TTTCTTTTCTTTTACCAATTTTGTGTAAGACACAGTCTTCTCAAAACCTTGTTTC	3235
DB	9563	TTTCTTTTCTTTTACCAATTTTGTGTAAGACACAGTCTTCTCAAAACCTTGTTTC	9621
QY	3236	TCTATTTTGTGTTTACTGTTTAAAGATCAAGTTCATTTCTTTGAGCTGCTCATAT	3295
DB	9622	TCTATTTTGTGTTTACTGTTTAAAGATCAAGTTCATTTCTTTGAGCTGCTCATAT	9681
QY	3296	TTTCTTACCTGAACCTTTGCAAGTTTGAAGTAACCTCAGTCAAGAGCTGCTATATG	3355
DB	9682	TTTCTTACCTGAACCTTTGCAAGTTTGAAGTAACCTCAGTCAAGAGCTGCTATATG	9741
QY	3356	TCCTCTTAAGAAGATTTAAAAAATTTAAAAA 3386	
DB	9742	TCCTCTTAAGAAGATTTAAAAAATTTAAAAA 9772	

RESULT 15  
 US-09-919-060-4





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QY 1859 CTAGATGATATCATGCCACAGTACTACTAATAAAGCGTCCAGTCACTGTAGAGCT 1918
Db 1814 CTAGATGATCATCATCCACAGCTCACTGAAAGAGCGGTCAACTGATATAGAGCC 1873
QY 1919 AATGATCATATTTATTTATTTATGAGACCATGCTATTAATTTATTTATTAATAT 1978
Db 1874 GTTAATCCATTTATTTATTTATGAGAGATTCCTTTTACTTATTTATTT---TATAT 1930
QY 1979 TTATATTAACCTCTTATGTACTTAACTCTTCTGTAAAGAGTCACTCTCTGTG 2038
Db 1931 TTATGTTAAACCTTATGTACTTAAACAT-----CTGTAA 1966
QY 2039 CCGAGAAAGAGTCACTTGTGAAGACTTTTATGCTACTCTAAAGATTTGCTGT 2098
Db 1967 AGGAGAAAGGCTCATCTTGTGAAGATTTTCACTGCTATTTTAAGATGT---CT 2021
QY 2099 GCTGTTAAGTTGAAACAGTTTATTTCTGTTTATTAACCAAGAGAAATGAGTTT 2158
Db 2022 TCGGGTTAAAGAGAAACAGTT---TTCTGTTTATTAATGAG-----TTT 2065
QY 2159 GACGCTTTTCTGAATTTCACTTATTTATTAAGACGAAAGTAA---AGATGTTG 2215
Db 2066 GACATCCCTTTTACTGAAATTTCACTTATTTATTAATTAAGAAACAAAGCGAAGATGTG 2125
QY 2216 AATACTTAAACATATCAACAAGATGCCAAATGCTGAAGTTT---ACACTGCGAT 2271
Db 2126 GATATTTAAATGCTGTCTCAGATGACAAATGCTGCAAGTTT---TTTGACACTATCGGG 2185
QY 2272 GTTCCAAATGATCTTCCATGATGATTAAGAAATGAAAGTAACTATGTTGAAATTTTAAAGTAC 2331
Db 2186 ATTTCTAGGTATCTTCCCTGGTGCATTAAGAAACTGACACTTCTTTCTTCTC 2245
QY 2332 TTTGGGTATTTTCTGTCATCA 2355
Db 2246 TGTAGCCACTGTGCTGGTAGAA 2269
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Search completed: April 24, 2004, 17:01:09  
Job time : 1323 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 07:25:26 ; Search time 8126 Seconds

(without alignments)  
12446.863 Million cell updates/sec

Title: US-08-064-271-11

Perfect score: 3387  
Sequence: 1 GTCACGAGACCTCCACAGAG.....GATTAAAAAAAAAAAAAG 3387

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estcov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gp\_est1:\*  
10: gp\_est2:\*  
11: gp\_hlc:\*  
12: gp\_est3:\*  
13: gp\_est4:\*  
14: gp\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vrl:\*  
28: gp\_gsei:\*  
29: gp\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437.2	42.4	2247	11	AK049923 Mus muscu
2	976.2	28.8	1201	13	BX363285 BX363285
3	887.4	26.2	997	9	AL583668 AL583668
4	814.8	24.1	968	13	BX370552 BX370552

5	728	21.5	810	9	AI971172	AI971172 wr26a04.x
6	718.8	21.2	2132	14	CD014050	CD014050 90138391
7	713	21.1	2793	11	AK046457	AK046457 Mus muscu
8	703.4	20.8	744	14	CD365731	CD365731 UI-H-FRT2
9	685.4	20.2	808	14	CB960307	CB960307 AGENCOURT
10	674.2	19.9	701	9	AL710848	AL710848 DKFZp686N
11	672.2	19.8	707	14	CA309056	CA309056 UI-H-FRT1
12	663.2	19.6	1473	29	AY415140	AY415140 Homo sapi
13	662	19.5	662	9	AL710813	AL710813 DKFZp686J
14	657.2	19.4	1448	29	AY415141	AY415141 Pan trogl
15	642	19.0	1448	29	AY415142	AY415142 Mus muscu
16	629	18.6	663	10	BG055155	BG055155 na302e05.
17	623	18.4	631	10	BE673090	BE673090 7d29b11.x
18	599	17.7	1766	14	CD014048	CD014048 90138112
19	571.4	16.9	573	12	BM129013	BM129013 if16d06.y
20	571.2	16.9	605	9	AL691944	AL691944 DKFZp333C
21	570.8	16.9	581	12	BM128780	BM128780 if16d06.x
22	566.4	16.7	612	14	CA308732	CA308732 UI-H-FRT1
23	565.6	16.7	606	9	AL691954	AL691954 DKFZp313D
24	565	16.7	1040	10	BE785396	BE785396 601478114
25	563.8	16.6	567	14	CB146285	CB146285 K-EST0201
26	548.8	16.2	1770	14	CD014049	CD014049 90138252
27	545	16.1	565	13	BQ100978	BQ100978 if12d09.y
28	544.2	16.1	602	9	AL712736	AL712736 DKFZp686K
29	540.6	16.0	559	13	BQ100700	BQ100700 if12d09.x
30	532.2	15.7	597	9	AL783660	AL783660 tu28a05.x
31	531.6	15.7	645	14	CE787487	CE787487 855389 MA
32	529	15.6	776	9	AV756509	AV756509 AV756509
33	507.2	15.0	949	12	BI689383	BI689383 603315826
34	506.4	15.0	1107	14	CK030311	CK030311 AGENCOURT
35	488.2	14.4	612	14	CB243167	CB243167 UI-CF-FNO
36	487.4	14.4	489	9	AL710680	AL710680 DKFZp686E
37	486.4	14.4	593	14	CE788077	CE788077 856797 MA
38	475.2	14.0	594	9	AI123006	AI123006 OK36C09.s
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41	464	13.7	522	9	AA825346	AA825346 oe63d06.s
42	454.2	13.4	473	12	BM988211	BM988211 UI-H-COO-
43	448.8	13.3	866	14	CA988090	CA988090 AGENCOURT
44	445.4	13.2	657	14	CF907989	CF907989 A0517D05-
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## ALIGNMENTS

RESULT 1  
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LOCUS 2247 bp mRNA linear HTC 20-SEP-2003  
DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length  
enriched library, clone:G630011G21  
product:prostoglandin-endoperoxide synthase 2, full insert  
sequence.  
ACCESSION AK049923  
VERSION AK049923.1 GI:26340647  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374

PUBMED REFERENCE AUTHORS	11042159 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komano, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	20530913 11076861 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
JOURNAL AUTHORS	5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL REFERENCE AUTHORS	6 (bases 1 to 2247) Aouchi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T., Horii, F., Imochi, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, K., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohmoto, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physiological and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers
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Db	801	AAATGAAATTCAGATATTTGATGAGAGATGTATCTCCACAGTCAAGATCTAGG	860	
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[illegible]

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RESULT 3
AL583668
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL583668      997 bp      mRNA      linear      EST 01-JUN-2003
AL583668 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
-cDNA clone CSODK012YH07 5-PRIME, mRNA sequence.
AL583668
AL583668.2   GI:31321840
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 997)
Li, W.B., Gruber, C., Jesse, J. and Polyses, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12952851.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 691.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSODK012CD04QPI&cluster=691.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation 1600
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Location/Qualifiers
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sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

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VERSION	BX370552.1	GI:30457926	
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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JOURNAL	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 9106 Evry cedex - France		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	Library was constructed by life technologies, a division of		
	Invitrogen. This sequence belongs to sequence cluster 691.r For		
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	Contact : Feng liang Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
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ACCESSION A1971172.1 GI:5767998  
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 810)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-ismail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/INL at:  
 www-bio.lnlnl.gov/bbrp/image/image.html  
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 /note="Organ: prostate; Vector: pTZ19-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI-CGAP\_Pz22 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

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 1 (bases 1 to 2132)  
 Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,  
 Au-Yang, J., and Stuve, L.L.  
 PCR isolation and cloning of novel splice variant mRNAs from known  
 drug target genes  
 Unpublished (2003)  
 CONTACT: Jin, P.  
 Incyte Corporation  
 3160 Porter Drive, Palo Alto, CA 94304, USA  
 Tel: 650 621 8639  
 Fax: 650 621 8965  
 Email: pjine@incyte.com.





**AUTHORS** Carninci, P., Hayashizaki, Y.  
**TITLE** High-efficiency full-length cDNA cloning  
**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)  
**MEDLINE** 99279253  
**PUBMED** 10349636  
**REFERENCE**

**TITLE** Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
**JOURNAL** Genome Res. 10 (10), 1617-1630 (2000)  
**MEDLINE** 20493574  
**PUBMED** 11042159  
**REFERENCE**

**TITLE** Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashtiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicillary sequencer  
**JOURNAL** Genome Res. 10 (11), 1757-1771 (2000)  
**MEDLINE** 20530913  
**PUBMED** 11076861  
**REFERENCE**

**TITLE** The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
**JOURNAL** Functional annotation of a full-length mouse cDNA collection  
**REFERENCE** Nature 409, 685-690 (2001)

**TITLE** The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
**JOURNAL** Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
**REFERENCE** Nature 420, 563-573 (2002)

**TITLE** 6 (bases 1 to 2793)  
**JOURNAL** Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furum, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, S., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyana, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Salto, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shigenaga, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akchira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physiolical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama-Kanagawa 230-0045, Japan (E-mail: genome-resgs@riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

**COMMENT** cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
Location/Qualifiers

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 AUTHORS  
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 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL  
 COMMENT  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
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 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bhs-riemail.nih.gov  
 Tissue Procurement: Dr. Stefan Hansson  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
 and advice from Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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## ORIGIN

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RESULT 10  
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DEFINITION  
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DKFZp686N0473.r1.686 (synonym: h1cc3) Homo sapiens cDNA clone  
AL710848  
ACCESSION  
AL710848.1 GI:19694203  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.  
REFERENCE  
EST (Duesterhoeft, et al.)  
JOURNAL  
Unpublished (1999)  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686N0473) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
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/clone="DKFZp686N0473"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: h1cc3)"  
/note="Vector: pT73-Pac; Site\_1: SfiI; Site\_2: SfiI; B:  
cDNA-collection"

## ORIGIN

Query Match 19.9%; Score 674.2; DB 9; Length 701;  
Best Local Similarity 99.3%; Pred No. 2.4e-135;  
Matches 698; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
631 GGAGCTCAACATGATGTTGCAATCTTTGCCCCAGACATTACGACACGATTTTCAAGAC 690  
1 GGAGCTCAACATGATGTTGCAATCTTTGCCCCAGACATTACGACACGATTTTCAAGAC 60  
691 AGATCTAAGCGAGGGCCAGCTTTTCACCAAGGGGCTGGGCGCATGGGCTGAATTAATCA 750  
61 AGATCTAAGCGAGGGCCAGCTTTTCACCAAGGGGCTGGGCGCATGGGCTGAATTAATCA 119  
751 TATTTACGGTGAACCTCTGGCTAGACAGCGTAAAGTGCCTTTTCAAGGATGAATAAT 810  
120 TATTTACGGTGAACCTCTGGCTAGACAGCGTAAAGTGCCTTTTCAAGGATGAATAAT 179  
811 GAAATATCAGATTAATGATGAGAGATGATCTCTCCCAAGTCAAAAGATCTCAGGACGA 870  
180 GAAATATCAGATTAATGATGAGAGATGATCTCTCCCAAGTCAAAAGATCTCAGGACGA 239  
871 GATGATCAACCTCCCTCAAGTCCCTGAGATCTAAGGTTGCTGGGGGAGAGAGTCTT 930  
240 GATGATCAACCTCCCTCAAGTCCCTGAGATCTAAGGTTGCTGGGGGAGAGAGTCTT 299  
931 TGGTCTGGGCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 990  
300 TGGTCTGGGCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359  
991 ATGTGATGCTTAAACAGGAGCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1050

Db 360 ATGGCATGTGCTTAAACAGAGACATCTGAAATGGGGTGATGACGATTTGTTCCAGACAG 419  
Qy 1051 CAGGCTAATAGTATAGAGAGACTATTAAGTTGATTTGAAGTTATGTCACACTT 1110  
Db 420 CAGGCTAATAGTATAGAGAGACTATTAAGTTGATTTGAAGTTATGTCACACTT 479  
Qy 1111 GAGTGGCTATCAGTCAACCTGAATTTGACCCAGAACTACTTTTCAACAAACAAATTCCA 1170  
Db 480 GAGTGGCTATCAGTCAACCTGAATTTGACCCAGAACTACTTTTCAACAAACAAATTCCA 539  
Qy 1171 GTACCAATGCTATGCTGCTGATTTAAACCTCTATCATCTGGGATCTCCCTTCGCC 1230  
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Qy 1231 TGACACCTTCAATTTGATGACCAAGATTAACACTATGACAGTTATCTACACACTC 1290  
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Qy 1291 TATATTGCTGGAACATGGAATTACCCAGTTGTTGAATCATTC 1333  
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RESULT 11  
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LOCUS  
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CA309056 707 bp mRNA linear EST 01-NOV-2002  
UI-H-F11-Die-1-15-0-UI.s1 NCI CGAP F11 Homo sapiens cDNA clone  
UI-H-F11-Die-1-15-0-UI 3', mRNA sequence.  
CA309056  
VERSION  
CA309056.1 GI:24472110  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 707)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
CONTACT: Robert Strausberg, Ph.D.  
Email: cga@bbs-r@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, Bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 550-627, >(TAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP F11"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP F11 is a normalized cDNA library constructed from  
a pool of 81 RNA samples from Alveolar Macrophages  
challenged with different treatments. The library was  
normalized according to Bonaldi, Lennon and Soares, Genome  
Research, 6:791-806, 1996. First strand cDNA synthesis was  
primed with an oligo-dT primer containing a Not I site.  
Double stranded cDNA was ligated to an EcoR I adaptor,  
digested with Not I, and cloned directionally into  
pT73-Pac vector. The oligonucleotide used to prime the

synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)<sub>18</sub> tail. The sequence tag for this library is GGGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG TISSUE=Human Lung Ateolar Macrophage TAG LIB=UI-H-F11 TAG\_SEQ=GGGCATGCCG"

Query Match 19.8%; Score 672.2; DB 14; Length 707;  
Best Local Similarity 98.7%; Pred. No. 6,4e-135;  
Matches 688; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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707 TCCCGCTCCGCGATAGATGATATCATCCACAGTACTACTATAAAGACGCTGCAGTAA 648  
1907 CTGTAGAGCTAATGATCATATTTATTTATTTATGAAACATGCTATTTATTTAAT 1966  
647 CTGTAGAGCTAATGATCATATTTATTTATTTATGAAACATGCTATTTAATTTAAT 588  
1967 ATTATTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 2026  
587 ATTATTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 528  
2027 GTACTCTGTGGGAGAAAGAGTATCTGTGTAAGACTTTATGCTACTACTATAA 2086  
527 GTACTCTGTGGGAGAAAGAGTATCTGTGTAAGACTTTATGCTACTACTATAA 468  
2087 GATTTTGTCTGTGCTGTATTAAGTTTGAACAGTTTATTTCTGTTTATTAACAGAGA 2146  
467 GATTTTGTCTGTGCTGTATTAAGTTTGAACAGTTTATTTCTGTTTATTAACAGAGA 408  
2147 GAAATGAGTTTGAAGTCTTTTACTGTAATTTCACTTATTTATTAAGAGAGAAATTA 2206  
407 GAAATGAGTTTGAAGTCTTTTACTGTAATTTCACTTATTTATTAAGAGAGAAATTA 348  
2207 AGATGTTTGAATCTTAAACATATCAAGATGCGAAATGCTGAAAGTTTTCACATG 2266  
347 AGATGTTTGAATCTTAAACATATCAAGATGCGAAATGCTGAAAGTTTTCACATG 288  
2267 TCGATGTTTCAATGATCTTCATGATGATGATGATGATGATGATGATGATGATGAT 2326  
287 TCGATGTTTCAATGATCTTCATGATGATGATGATGATGATGATGATGATGATGAT 228  
2327 AGTACTTTGGGTATTTTCTGTCATCAAC-AAAAAGGTATCGTGCATTTTAAATG 2385  
227 AGTACTTTGGGTATTTTCTGTCATCAACAAAAAGGTATCGTGCATTTTAAATG 168  
2386 AATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2445  
167 AATATTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 108  
2446 CAATATTTGAAATTTCTPAATTCATGAGGTGAAATCACTGTAAGCTGTGTTGATTT 2505  
107 CAATATTTGAAATTTCTPAATTCATGAGGTGAAATCACTGTAAGCTGTGTTGATTT 48  
2506 CTAAAGTTATTAACCTGTACATATACCAAAAAA 2542  
47 CTAAAGTTATTAACCTGTACATATTCACAAAAA 11

RESULT 12  
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LOCUS Homo sapiens PTGS1 gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY415140  
VERSION AY415140.1 GI:39771099  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
gene  
ORIGIN

Query Match 19.6%; Score 663.2; DB 29; Length 1473;  
Best Local Similarity 66.7%; Pred. No. 5.2e-133;  
Matches 947; Conservative 0; Mismatches 473; Indels 0; Gaps 0;

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5 TCATGCGCTGCTACTCATCATGCTGCTCAACCTTATCCCATGCTCCCATCTCAACT 64  
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510 TTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569  
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570 CTGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 629  
185 CAGATGCCAGCTCTGCGCCGCCGCTTCTGCTGATGATGATGATGATGATGATGATGAT 244  
630 AGGCTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689  
245 AAGGACCAACCTCATGTTGCTTCTTTCACAAACATTCACCAACAGATTCCTTCAAA 304  
690 CAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749  
305 CTTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 364  
750 ATATTTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 809  
365 ACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424  
810 TGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 869  
425 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484  
870 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929  
485 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 544  
930 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Satsky,J.J.,  
Adams,M.D. and Cargill,M.  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
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Db      665 CCCGCTCATCTCATAGGGAGACCAATCAAGATTGTCATGAGAGAGTACCTGACAGAGC 724
QY      1110 TGAAGTGTATCACTTCAAACTGAAATTTGACCCAGAACTACTTTTCAACAAACATTC 1169
Db      725 TGAAGTGTATTTCTCGAGCTGAATTTGACCCAGAGCTGCTTTGGTGTCCAGTTCC 784
QY      1170 AGTACCAAAATCGTATTTGCTGCTGAATTTAACACCTCTATCACTGAGCATCCCTTGTGC 1229
Db      785 AATACCCCAACCGCATTCAGATGAGATTTCAACATCTCTACACTGTGACCCCTCATGC 844
QY      1230 CTGACACTTTCAAATTCATGACCCAGAAATTCACATTCACAGTTTATCTACACAGACT 1289
Db      845 CTGACTCTTTCAGAGTGGGCTCTCCAGAGAGTACAGCTACAGCAGTTTCTTGTCAACACT 904
QY      1290 CTATATTTGCTGAACATGAAATTTACCCAGTTTGTGATCATTCACACAGGCAATTTGCTG 1349
Db      905 CCAATGTTGCTGAGCTATGGGGTTGAGGCTCTGTTGATGCTCTTCTTCGCCAGATTGCTG 964
QY      1350 GCAGGCTGCTGCTGTGATGAGAAATGTTCCACCCGAGTACAGAAATGATCAAGGCTTCCA 1409
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QY      1470 TGAAGCCTTATGATATCTTGAAGAACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGTGG 1529
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QY      1650 AAGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1709
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RESULT 13
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LOCUS     DKF2p686J1373.F1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION
  DKF2p686J1373 5', mRNA sequence.
ACCESSION
  AL710813
VERSION   AL710813.1 GI:19694168
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 662)
  Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and

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TITLE  
 JOURNAL  
 COMMENT

Wiemann, S.  
 Est (Duesterhoeft, et al.)  
 Unpublished (1999)  
 Contact: MIPS

MIPS  
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
 consortium of the German Genome Project.

No sequence available.  
 This clone (DKF2p686J1373) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

#### FEATURES

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#### ORIGIN

Query Match 19.5%; Score 662; DB 9; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 1e-132;  
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1024 GGGTGTGAGCACTTGTTCAGACAGCAGGCTTAATCTGATGAGAGACTATTAAGAT 1083
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QY      1084 TGTGATGAGAAATTTATGTCACACTTGTGAGTGTGCTATCACTTCAACTGAATTTGACCC 1143
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QY      1324 TGAATATTTACACAGCAATTTGCTGCGAGGTTGCTGTGTGATGAGAAATGTTCCACCCG 1383
Db      301 TGAATATTTACACAGCAATTTGCTGCGAGGTTGCTGTGTGATGAGAAATGTTCCACCCG 360
QY      1384 AGTACAGAAAGTATACACAGCTTCAATGATGACAGAGCAGAGCAAGTAATACAGATCTTT 1443
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QY      1444 TATAGTATCCGCCAAACGCTTTATGCTGAGAGCCCTATGATCAATTTGAAGAACTTACAG 1503
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QY      1504 AGAAAAAGAAATGTCTGCGAGAGTTGGAAGCACTTATGCTGACATGATGCTGTGAGGCT 1563
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Db 1384 TCCGTGTGCCGATGC 1399

RESULT 15  
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 genomic survey sequence.  
 ACCESSION AY415142 1448 bp DNA linear GSS 17-DEC-2003  
 VERSION AY415142  
 KEYWORDS AY415142.1 GI:39771101  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (bases 1 to 1448)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Interfing nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 TITLE Science 302 (5652), 1960-1963 (2003)  
 JOURNAL  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1448)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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 Matches 924; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 774 GACAGCGTAACAGCGCTTTTCAAGATGAGAAAAATATATGATATGATGAG 833  
 Db 364 GACAGTATCACTTGGGCTTTTCAAGATGAGAAAAATATATGATATGATGAG 423  
 QY 834 AGATGATCTCCCACTGCAAGATATCTCAGCAGATATATCTACCTCTCAAGTC 893  
 Db 424 AGGTATCCCACTTCCGTGAGACAGGCGTCCGTGATATGCGTATCCACCAAGGTGTC 483  
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 Db 544 TCTTCTCAGATCTGGCTGTGGGGCAGAGGCTTTTGTCTGTGGCTGTGATGA 603  
 QY 1014 ATCTGAAAGGCTGATGAGCAGTGTTCAGACAGAGGCTTAATCTGATAGAGGA 1073  
 Db 604 ATCCAGGTGGATGATGAGAGGCTTCCAGACCACTCGCTTATCTTATAGAGAAA 663  
 QY 1074 CTATTAAGATTTGATTTGAAGATTTATGTCACACTTGAAGTGTATCACTTCAACTGA 1133  
 Db 664 CCATCAAAATTTGATTTGAGAGATGTCAGACACTTGAAGTGTATTTCTGACGTCA 723  
 QY 1134 AATTGACCCAGAACTACTTTTCAAGAAATTTCCAGTACCAAAATGATTTGCTGTG 1193  
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 Db 1144 CTGTGAGCTGATCTGCTTCTGTGAAAGAGCTGAGAGTGAACACTTATGATG 1203  
 QY 1614 AACCATGATGAAGTGAAGCACTTCTGTAAGAGACTTATGATGATGATGATG 1673  
 Db 1204 AACCATGATGAAGTGAAGCACTTCTGTAAGAGACTTATGATGATGATGATG 1263  
 QY 1674 GTTCTCTGCTTCACTGAGAGCACTTTTGTGAGAGAGTGGTTTCAATATCA 1733  
 Db 1264 GTTCTCTGCTTCACTGAGAGCACTTTTGTGAGAGAGTGGTTTCAATATCA 1323  
 QY 1734 ACATGCTCTCAATTCATGCTCTCATCTGCAATTAACGTAAGAGGCTGCTTACTTCA 1793  
 Db 1324 ACATGCTCTCAATTCATGCTCTCATCTGCAATTAACGTAAGAGGCTGCTTACTTCA 1383  
 QY 1794 TCAAGTTCAGAT 1807  
 Db 1384 TCCGTGTGCCGAT 1399

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